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US-08-779-801-5
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US-09-034-985-1
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5: /cgn2_6/ptodata/l/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/l/ina/6_COMB.seq:*
7: /cgn2_6/ptodata/l/ina/PCTUS_COMB.seq:*
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 PCT-US93-0651-7 Sequence 7, Application PC/TUS9306251 Sequence 7, Application PC/TUS9306251 SEGNERAL INFORMATION: TITLE OF INVENTION: Trivalent Synthes TITLE OF INVENTION: Stereospecific A. TITLE OF INVENTION: Stereospecific A. NUMBER OF SEQUENCES: 93 CORRESPONDENCES: 93 CORRESPONDENCES: 93 CORRESPONDENCES: 93 CORRESPONDENCES: 93 CORRESPONDENCES: 93 CORRESPONDENCES: 93 COUNTRY: USA ZIP: 11530 COMPUTER: IBW PC COMPATION: MEDIUM TYPE: Floppy disk COMPUTER: THE PC COMPATION: MEDIUM TYPE: Floppy disk COMPUTER: THE PC COMPATION: MEDIUM TYPE: Floppy disk COMPUTER: PatentIn Release #1.0, W CONTRY: USA ZIP: 11530 COMPUTER: PSTENTION: PCT/US93/06251 FILING DATE: 19930630 CLASSIFICATION: NUMBER: 9586 TELEPHOME: 516-742-4343 TELEPHOME: 516-742-4343 TELEPHOME: 516-742-4366 TELERAX-150-05XER NUMBER: 9586 TELECOMMUNICATION INFORMATION: TELEPHOME: 516-742-4366 TELERAX-150-05XER NUMBER: 9586 TELECOMMUNICATION INFORMATION: TELEPHOME: 3090-Dase pairs TYPE: NUCLEIR SOULDES TYPE: NUCLEIR SOULDE TYPE: DUCLEIR SOUL	Query Match Best Local Similarity Matches 535; Conserv Qy 352 aggogacactggC Qy 590 AGGCGAAACCTAAC

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COMPUTER READSLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
COMPUTER: 180 FC COMPATIBLE
COMPUTER: 180 FC COMPATIBLE
SOFTWARE: ASCIT
CURRENT APPLICATION DAY:
APPLICATION NUMBER: 05/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
FEGISTRATION NUMBER: 39,911
FEGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                        REFERENCE DOCKET NUMBER: 95700/437
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 46:
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LENGTH: 9960
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Best Local Similarity 45.29
Matches 170; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
RY: U.S.A.
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HYPOTHETICAL:
US-08-822-586-46
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Fatent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT:
APPLICANT: WALLIO TELENTI
TILLE OF INVENTION: AN EMBCAB OPERON OF MICOBACTERIA AND TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDERSS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STATE: NEW YORK
STATE: NEW YORK
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       Length 9960;
Score 46.4; DB 5; Length 9
Pred. No. 0.047;
0; Mismatches 206; Indels
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GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Mary C.

APPLICANT: BETLACH, Mary C.

APPLICANT: TANG, Li

TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 30062200120

CURRENT APPLICATION NUMBER: US/09/320,878A

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER PILING DATE: 1998-08-28

EARLIER PILING DATE: 1998-06-06

EARLIER PILING DATE: 1998-06-06

EARLIER FILING DATE: 1999-02-06

EARLIER FILING DATE: 1999-02-06

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1998-06-28

EARLIER FILING DATE: 1998-09-22

EARLIER FILING DATE: 1998-09-22

EARLIER FILING DATE: 1998-09-28

EARLIER PILING DATE: 1998-09-28

EARLIER PILING DATE: 1998-09-28

EARLIER FILING DATE: 1998-09-28 911 AGACCITCGGCACCCACAAGAICGAGACCGAGAAGATCGAGAACGCCATCGGCGAGGTCT 977 aaccccagcagcgcatccacgtgtcagaggagcagctgcagctctactggg 1027 TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE Length 1693; AGACCGCCGTACGCCACTTCGGCCGCGAGCTGCCGGACTTCACCTGGG 741 Query Match
3.0%; Score 42.2; DB 5; Length 1
Best Local Similarity 48.9%; Pred. No. 0.27;
Matches 113; Conservative 0; Mismatches 118; Indels FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: UG/09/320,878A
CURRENT APPLICATION NUMBER: UG/09/320,878A
EARLIER APPLICATION NUMBER: CIP OF 09/11/9.08
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-08
EARLIER FILING DATE: 1999-06-06
EARLIER FILING DATE: 1999-06-06
EARLIER FILING DATE: 1999-06-06
EARLIER APPLICATION NUMBER: GO/110,139
EARLIER APPLICATION NUMBER: GO/10,880
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: GO/10,880
EARLIER APPLICATION NUMBER: GO/10,880
EARLIER PILING DATE: 1998-05-28
EARLIER PILING DATE: 1998-05-28
INUMBER OF EQ ID NOS: 34
SOFTWARE: PATGUIL VET: 2.0
SEQ ID NO 23
LIENGTH: 1693 RESULT 4 US-09-320-878-22/c Sequence 22, Application US/09320878A Patent No. 6117659 TYPE: DNA
CRGANISM: Streptomyces venezuelae
US-09-320-878-23 917 791 dd ŏ Qγ g δλ g

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GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Hong Zhan
APPLICANT: Hong Zhan
APPLICANT: HONG Zhan
APPLICANT: HON MUNISHNE MODULATION OF FADD EXPRESSION
TITLE OF INVENTION: ANTISHNE MODULATION OF FADD EXPRESSION
TITLE OF INVENTION: WUMBER: US/09/357,072
CURRENT APPLICATION UNMBER: US/09/357,072
CURRENT FILING DAIE: 1999-07-19
NUMBER OF SEQ ID NOS: 87
LENGTH: 1701
  Length 3292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 2.8%; Score 40; DB 5; Length 1701; Best Local Similarity 49.1%; Pred. No. 0.88; Matches 106; Conservative 0; Mismatches 110; Indels
                                               Indels
Score 41.6; DB 5; Pred. No. 0.45; 0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09357072
Patent No. 6015712
    Query Match
Best Local Similarity 46.3%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (145)..(771)
US-09-357-072-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-357-072-1
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LENGTH: 3292
FYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-320-878-22

2.0

SOFTWARE: Patentin Ver. SEQ ID NO 22 LENGTH: 3292 ó

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92 aatgogtogacccccggctgtccgtgagtcccccttcgctgcgggacctgctgccccgcs, 151
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                                                          152 cagogagotgottogagaggtggcocattotoggogggoggcoggoggaggoggoocg
                                                                                                                                                                                                                                                                                                                             MODULATORS OF THE FUNCTION OF FAS RECEPTORS AND OTHER PROTEINS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%; Score 40; DB 6; Length 170
49.1%; Pred. No. 0.88;
tive 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CUSTIVARE: Patentin Release #1.0, Version #1.30 (EPO)
CUSTENT APPLICATION NUMBER: PCT/US96/10521
                                                                                                                                      212 ggggtcccgg@gctctggggactttctactcatct 247
                                                                                                                                                                422 GGGAAGAAGACCTGTGTGCAGCAITTAACGTCATAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9610521 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.1<sup>s</sup>
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
1.,768
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MOLECULE TYPE:
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; LOCATION:
PCT-US96-10521-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 agtgggaagaggcccgcgccctgggccgggcagtcaggatgctgcagcgcctagaagagc 91
                                                                                                                                                                                                                                                              APPLICANT: METT, IGOR
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 1701;
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                                                                                                                                                                APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
APPLICANT: WEINWIRZEL, Henry
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VARFOLOMEEV, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 40; DB 6; Ler
49.1%; Pred. No. 0.88;
tive 0; Mismatches 110;
212 ggggtcccggcggctctgggggactttctactcatct 247
                                    422 gggaagaacctgtgtgcagcatttaacgtcatat 457
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WALLACH=16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
ILING DATE: 112692
FILING DATE: 19-EBB-1995
PRIOR APPLICATION DATA:
FILING DATE: 10-TEB-1995
APPLICATION DATA:
APPLICATION DATA:
ILING DATE: 16-JUL-1995
ATTORNEY AGENT INFORMATION:
RABELSTRAIN NUMBER: 25-618
REFERENCE/DOCKET NUMBER: WALLACTELEPHONE: (202) 628-5197
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION DATA:
TELEFORMUNICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 1701 DATE PAIR
STRANDENESS: SINGLE
                                                                                                                              Sequence 1, Application PC/TUS9516542 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.18
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                 SIREET: 415 CTIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
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; LOCATION:
PCT-US95-16542-1
                                                                                            RESULT 6
PCT-US95-16542-1
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NEGOTA 1. APPLICATION US/08972631
Sequence 1, APPLICATION US/08972631
Sequence 1, APPLICATION GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: BAWAINS, Phillip T.
ITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
SIREET: 2730 Sand Hill Road
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Bawkins, Phillip Thomas
APPLICANT: Baselmann, Sylvia
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: DAMPENS: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
ZIP: 1033-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
212 ggggtcccggcggctctgggggactttctactcatct 247
                              NAME: Abrams, Samuel B
RECISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-493-4935
TELEPA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-917-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILLING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                             RESULT 8
10S-08-916-917-1/c
Sequence 1, Application US/08916917
Patent No. 5856132
     δλ
                                                 g
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELECOMENUICATION INFORMATION:
TELEPHONE: (415)854-3660

TELEFAX: (415)854-3694 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4692 base pairs

TYPE: nucleic acid

STRANDEDNESS:

unknown

TOPOLOGY:

; MOLECULE TYPE: CDNA US-08-972-631-1

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-20N-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,631

ZIP: 94025 COMPUTER READBLE FORM: MEDIUM TYPE: FIDPPY disk COMPUTER: IBM PC COMPATIBLE

CITY: Menlo Park STATE: California COUNTRY: USA

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  Length 4692;
Query Match 2.7%; Score 38.4; DB 3; Length 4: Best Local Similarity 50.9%; Pred. No. 2.8; Matches 116; Conservative 0; Mismatches 111; Indels
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1833 GCTTGGGGCTGGGGCAGCGGGGAG-CCCTGGGCCCGGGACGGGGGGCAGGGTGGTG 1775

Db δŏ g

4 getetggeggtggeecegtgggggegaeagtgggaagaggeeeggggeetggggeeg

Length 4692;

Score 38.4; DB 3; Length 4 Pred. No. 2.8; 0; Mismatches 111; Indels

2.7%;

Query Match 2.7% Best Local Similarity 50.9% Matches 116; Conservative

64 gtcaggatgctgcagcgcctagaagagcaatgcgtcgaccccggctgtccgtgagtccc 123

1714 recassersessas de receses de concesas de la recassa de la 1655

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124 cettegetgejggacetgetgeecegeacagegeagetgettegagaggtggeecattet 183

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1774 Tocadosescriecas de cresces ecceses de aceses de consecuences es en 1715
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4 getetggcggtggcccgtggggggggacagtgggaagaggcccgcgccctgggccgggca 63
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1654 ATCCTGTTGAACTTCTGCCCGGGCCGGCGGTGGCCCCGGCGCTCGTGG 1607 184 cggcgggcgggcggaggcgcccggggggtcccggcggctctggg Sequence 1, Application US/08972629 Patent No. 5859201. GENERAL INFORMATION: APPLICANT: Stephens, Len RESULT 10 US-08-972-629-1/c

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2730 Sand Hill Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                     ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94025
COMPUTER READABLE FORM:
                          Menlo Park
Californía
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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Matches 116; Conserv
                                                                    USA
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US-08-972-630-1
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                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7%; Score 38.4; DB 3; Length 4692; 50.9%; Pred. No. 2.8;
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APPLICANT: Hawkins, Phillip T.

TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-972-630-1/C
Sequence 1, Application US/08972630
Sequence 1, Application US/08972630
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Stephens, Palllip T.
APPLICANT: GENERAL REGULATED
ITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESCONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                     ZIE: 94025
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: PATEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27'-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hallinin, Albert P.
REGISTRATION NUMBER: 25,277
REPERRING-POCKET NUMBER: 8549-0005-999
TELEPHONE: (415)854-360
TELEPAN: (415)854-360
TELEPAN: (415)854-360
TELEFAX: (415)854-360
TELEFAX: (415)854-360
TELEFAX: (415)854-360
TELEFAX: (415)854-360
TELEFAX: (415)854-369
TELEFAX: (415)854-369
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Best Local Similarity 50.9
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: un; MOLECULE TYPE: US-08-972-629-1
                                                                                                                                                                                        COUNTRY:
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COMPUTER: REALABLE FORM:
MEDINATURE: FLORY disk
COMPUTER: REALABLE FORM:
MEDINATURE: FLORY disk
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MEDINATURE: FLORY disk
COMPUTER: REALABLE FORM:
MEDINATURE: MATCH REALABLE #1.0, Version #1.30
SOUTHAND BATE:
MEDINATURE MATCH REALABLE #1.0, Version #1.30
SOUTHAND BATE: US-06/972.630
FLING DATE: Z7-JUN-196
FLING DATE: Z7-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.4; DB 5; Length 4 Pred. No. 2.8; 0; Mismatches 111; Indels
                                    RESULT 14
US-08-680-506-5/c
Sequence 5, Application US/08680506C
Patent No. 6008013
GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION:
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 196-07-08
EARLIER APPLICATION NUMBER: 60/021,672
SOFTWARE: PATENTY DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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50.2%;
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Best Local Similarity 50.9%;
Matches 116; Conservative
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Best Local Similarity 50.2%
Matches 120; Conservative
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COGANISM: Gallus gallus
US-08-680-506-5
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| Sequence 1, Application US/09225170
| Patent No. 6017763
| GENERAL INFORMATION:
| APPLICANT: Stephens, Len
| APPLICANT: Braselmann, Sylvia
| APPLICANT: Braselmann, Sylvia
| APPLICANT: Braselmann, Sylvia
| TITLE OF INVENTION: G-BETA-GAMA REGULATED
| TITLE OF INVENTION: G-BETA-GAMA REGULATED
| UNDER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Pennie & Edmonds, LLP
| STREET: New York
| CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 cggcggcggccggcggaggcggcccgggggtcccggcggctctggg
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-210-1996
CLASSIETCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPRATION NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastEMD for Windows
CURBENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.4;
Pred. No. 2.
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Best Local Similarity 50.9%;
Matches 116; Conservative
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CLASSIFICATION:
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223 ggctctggggactttctactcatctacctggccaatctg-gaggccaagagcaggcaggt 281
                      163 cttcgagagatggcccattctcgggcggccggcgggcggaggcgcccggggtcccggc 222
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2.7%; Score 38.2; DB 5; Length 1347;
Best Local Similarity 50.2%; Pred. No. 2.2;
Matches 120; Conservative 0; Mismatches 118; Indels 1
                                                                                                                                        RESULT 15
US-08-68/C
Sequence 8, Application US/08680506C
Patent No. 6008013
GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENY APPLICATION NUMBER: US/08/680,506C
CURRENY FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
BARLIER FILING DATE: 1996-07-08
SEALIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 8
LENGTH: 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-8
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Search completed: December 7, 2000, 13:40:43 Job time: 27492 sec

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7, 2000, 18:06:44; Search time 152.48 Seconds (without alignments) 3503.360 Million cell updates/sec
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1 atggctctggcggtggccc......cccaggaccctgcccggcc 1422
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Perfect score:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Nucleotide sequenc	Gene encoding a su	Mycobacterium smeg	Human adenosine Al	Contig 004 from co	S. venezuelae deso	Contig 003 from co	S. venezuelae deso	S. venezuelae deso	Human FADD protein	FADD (Fas-associat	Human fishboy G-pr
SUMMARIES	ΩĬ	X89079	A10594	V58939	X53491	256005	287290	256004	287284	287319	X08910	T39397	239042
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	Query Match Length DB ID	3090	10732	0966	114955	1693	1140	3291	12441	13613	1582	1642	1170
dР	Query	23.9	3.4	3.3	3.2	3.0	2.9	2.9	2.9	2.9	2.9	2.9	2.9
	Score	340	48	46.4	46	42.2	41.6	41.6	41.6	41.6	41.4	41.4	41.2
	Result No.		7	m	4	0	o U	0 7	80	6	10	11	c 12

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ALIGNMENTS

IAT; tyrosine kinase; linker for activation of T cell; TCR; human; T-cell receptor; TCR signalling pathway; neoplasia; inflammation; hypersensitivity; allergy; microbial infection; genetic disease; autoimmune disease; graft rejection; modulator; Cbl; ss. Linker for activation of T cell protein used to, e.g. screen for modulators of T cell signalling (USSH) US DEPT HEALTH & HUMAN SERVICES. Nucleotide sequence of human Cbl. X89079 standard; DNA; 3090 BP 98WO-US27400 97US-0068690 (first entry) Samelson LE, Zhang W; WPI; 1999-418925/35. P-PSDB; Y27126. W09932627-A2. Homo sapiens. 23-DEC-1997; 23-DEC-1998; 01-JUL-1999. 14-SEP-1999 x89079;

The invention relates to a protein tyrosine kinase substrate LAT (linker for activation of reals) protein. Modulation of interaction between LAT and the T-cell receptor (TCN) affects the TCR signalling pathway. LAT is a substrate for tyrosine kinases and becomes phosphorylated after TCR engagement, resulting in recruitment of other signalling molecules. LAT is used to identify and test (art)agonists of tyrosine kinase signalling pathways. i.e. modulation of interaction between tyrosine kinase signalling pathways. i.e. modulation of interaction between these ligands and other members of the pathway, including identification of downstream signalling proteins, particularly in immune system cells. These modulators are potentially useful as drugs and diagnostic agents, particularly for diseases that involve undesirable cell proliferation, differentiation, diseases that involve undesirable cell proliferation, differentiation, alleray, microbial infection, mechanism inflammation, hypersensitivity, alleray, microbial infection, mechanism inflammation, hypersensitivity, are trajection of LAT. Nucleic acid that encodes LAT or its fragments, are used to identify homologous sequences in other species; to detect the control of th potentially more specific and less toxic than known immunosuppressants such as cyclosporin. The present sequence represents the nucleotide 12A; 125pp; English human Cbl Disclosure; Fig sednence $\overset{\alpha}{\times}\overset{\times}{\times}\overset{\circ}{\circ}{\circ}\overset{\circ}$

Sequence 3090 BP; 757 A; 840 C; 764 G; 729 T; 0 other;

ó 1069 gttactgctgatgggaacattctccagacaatccctcacaataaacctctctccaagca 1129 gacctgactgagctcggccaggcagaaccccagcagcgcatccacgtgtcagaggagcag 1011 649 471 531 591 829 651 711 949 891 Gaps aggogacagotggocaagotggocatcatctcagocacatgoacgcagagotgcacgca ctettecceggggcaaagtactgtggacacatgtaccagetcaccaaggeceegecac atctttccaagtggactctttcagggagacacatttcggattactaaagcagatgctgcg accttctggagggaaagttgcggagcccggtgtgtgctgccctgggctgagtttgagtcc ctcctgggcacctgccaccctgtggaaccaggctgcacagccctggccttgcgcaccacc getetacatgaagtgeateceateagttetgggetggaggeeatggetetgaaateeact tttcagccatggccaacactcctcaagaactggcagctcctggcagtcaaccacccaggc tttcagccctggtcctctttgctcaggaattggaacagccttgctgtaactcatcctggc tacatggccttcctcacctatgatgaggtccaagagcgtctgcaggcctgcagggacaag cctggcagttatatatctccggctgagctgtactcgtctgggtcagtgggctattgggtat gaattttggagaaaagcttttggggaaaagacaatagtcccttggaagagctttcgacag attgacctcacctgcagcgggcacgtgtccatcttcgagttcgacgtcttcaccaggctc gtgagetcagatggeageateetgeagaceateeetgeeaacaaeeceetgteeeaggtg ctcctggagggacagaaggacggcttctacctctacccagatggaaagacccacaaaccca ccaggcagttacatcttccggcccagctgtactcgcctggggcagtgggccatcggctat ö Length 3090; Indels Score 340; DB 20; Pred. No. 3.3e-64; 0; Mismatches 325; 23.9%; 62.2%; Conservative Similarity Local Simmes 535; Query Match Best Loca Matches 472 830 652 890 950 1010 1070 1130 352 590 412 650 710 770 592 832 532 712 892 952 g Q. δ g Q g g ò δ Db 9 q 8 QQ δ Db Š β δ ga à

This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant. gatotgactggottatgtgaaccaactccccaagaccatatcaaagtgacccaggaacaa 1249 1370 tggcaggaatcagaaggtcagggctgtcctttctgccgatgtgaaattaaaggtactgaa 1429 the improvement ctgcagctctactgggccatggactccacatttgagctctgcaagatctgtgctgagagc aacaaggatgigaagattgagccgtgcgggcacctgctctgcagctgctgcctggctgc gataaggatgtaaagattgagccctgtggacacctcatgtgcacatcctgtctacatcc tggcagcactcggacagccagacctgcccttctgccgctgcgatcaaggctgggag tatgaattatactgtgagatgggctccacattccaactatgtaaaatatgtgctgaaaat Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other; ds. cellulose production; increase yield; equipment - for a in a plant body Gene encoding a subunit of cellulose synthase. A gene encoding a cellulose synthetic e in the amount of cellulose synthesised Claim 2; Page 14-21; 32pp; Japanese. 1211 1430 occatogtggtagatccgtt 1449 DNA; 10732 BP 98JP-0239998 98JP-0239998 (first entry) 1192 gccgtgagtatctaccagtt (MIZU/) MIZUNO K. (OJIP) OJI PAPER CO. Cellulose synthase; 2000-342371/30. JP2000060568-A. A10594 standard; Vigna angularis 26-AUG-1998; 29-JUN-2000 26-AUG-1998; 29-FEB-2000. WPI; 2000 P-PSDB; A10594; 1012 1310 1132 A10594 셤 δ g QΥ 원 δŽ g

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Length 9960;

Score 46.4; DB 19; Pred. No. 0.28;

Sequence 9960 BP; 1389 A; 3592 C; 3360 G; 1618 T; 1 other;

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cgtcaccggcaccgaggtcggcacggaaggcggcaccacagctgccgcggggcatcaacgg gtcagaggagcagctgcagctctactgggccatggactccacatttgagctctgcaagat

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This is the DNA sequence of the Mycobacterium smegmatis embCAB operon, which determines resistance to the antimycobacterial drug chambulot (FMB). It includes the embA, embC and embD genes that encode proteins (see W13052-64) which are the trarget of action of M. smegmatis for EMB. To identify genes conferring EMB resistance, a genomic library from a high level EMB-resistant mutant of M. smegmatis was introduced into wild-type M. smegmatis mc2155. Four overlapping cosnids were identified which conferred a resistant phenotype. The minimum size fragment capable of conferring EMB resistance was 9 kD (plIMM9). plMM99 plus 7 kD upstream M. Smegmatis sequence was dequences revelaing 3 homologous open reading frames (embC, embB, embB) and 4 additional potential coding regions. Wild-type and mutated embCAB nucleic acid sequences are useful as probes used in the diagnosis of drug-resistant mycobacteria to to determine the susceptibility of mycobacteria to EMB. The nucleic acids are also useful in the treatment of mycobacterial infections; anti-DNA or anti-RNA sequences can be administered to inhibit embCAB operon mRNA activity (claimed). The invention additionally provides for the use of embCAM operon models acid sequences as vaccines, or to improve existing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wild type and mutated sequences of Mycobacterium embCAB operon useful to e.g..identify ethambutol-resistant mycobacterial strains and produce antisense sequences to treat mycobacterial infections
                                                     Drug resistance; antibiotic resistance; antimycobacterial; ethambutol; embCAB operon; infection; vaccine; therapy; ds
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               Mycobacterium smegmatis embCAB operon.
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P-PSDB; W73055-57.
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The specification describes antisense oligonucleotides (X52869-X55271)
directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
initiation codons, genomic flanking regions, intron-exon borders, the
initiation codons, genomic flanking regions, intron-exon borders, the
5'-end, the 3'-end and the juxta section between coding and non-coding
regions and all segments of RNAs encoding proteins associated with one
or more diseases, conditions or mixtures. The antisense oligonucleotides
oligonucleotides (specifically X55180-74. These multiple target
treatment of diseases and conditions. Typical diseases and conditions
are those associated with impaired respiration and inflammation,
allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
allergiatory disfress syndrome, pain, cyptic fibrosis, pulmonary
pypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
bulmonary disease (COPD), and cancers such as leukemias, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute asthma, allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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  ctgtgctgaggagcaacaaggatgtgaagattgagccgtgcgggcacctgctctgcagctg
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                                                                                                               Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
carcinomas e.g.:colon cancer, breast cancer, lung cancer, pancreatic cancer, heptacocillular carcinoma, Kidney cancer, melanoma, heptatic metastases, as well as all types of cancers which may metastasize or metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                    13 gtggccccgtggggggggacagtgggaagaggcccgcgccctgggccgggcagtcaggatg 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 004; ketclide; SAM synthase; S-adenosylmethionine synthase; hydroxylase;
                                                                                                       Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                       Db 104201 gggccgggcsmnndnncgggccgggcsnnndnnccgcbggccbggcgcgccggccg
                                                                                                                                                                                                                                                                                       Db 104141 gtcgggccgggcsnnndnncgtcgggccgggcsnnndnngtcgggccgggcsnnndnntc
                                                                                                                                                                                                                                                                                                                                   73 ctgcagcgcciagaagagcaatgcgtcgaccccggctgtccgtgagtccccttcgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             104261 gaccgsnnndinnccgcbggccbgggcgcgccggccgggccgnnndnnccgcbggccb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccggcggagycggccccggggggtcccggcggctctgggggactttctactcatctacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gocaatotggaggccaagagcaggcaggtggccgcgctgctgctccccgggggccgaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104381 dnnccgcbggccbggcgcgccggccggsnnndnnccgcbggccbggcgcgccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104441 gaccgsnnndnnccgcbggccbggcgcgcgccgccgccsnnndnnccgcbggccbgggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 104561 gcgccgccgsnnndnnccgcbggccbggcgcgccgccsnnndnnccgcbggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 104621 cgcgccgcsnnndnnccgcbggccbgggcgcgccgsnnndnnccgcbggccbggcgcgc
                                                                                                                                                                                                                                                                                                                                                                                                                       agtgccaacgacgactcttccgggcgggctccagactcaggcgacagctggccaagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 gecateatetteagecaeatgeaegeagagetgeaege---aetetteeeeggggeaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104501 egecgecggesnnndnneegebggeebggegegegegeegeggsnnndnneegebggeebgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 104681 csnnndnnccgcbggccbggcgcgcsnnndnnccgcbggccbgggcgcgsnnndnnccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgggcacgtgiccatcttcgagttcgacgtcttcaccaggctctttcagccatggccaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 tactgtggacacatgtaccagctcaccaaggcccccgcccacaccttctggagggaaagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              004 from cosmid pKOS023-27 from Streptomyces venezuelae.
                                                                                                                                                                   DB 20; Length 114955;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            405;
                                                                                                                                                                3.2%; Score 46; DB 23.5%; Pred. No. 0.53; ive 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 104801 dnnccgcbgggccbgggsnnndnnccgcbggc 104831
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 218, Conserv
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This is contig 004 from the recombinant cosmid pKOSO23-27 DNA sequence (see 256001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to che narbonolide polyketide synthase (PKS). The invention relates to common sequence for a narbonolide PKS.

CC recombinant DNA containing a coding sequence for a narbonolide PKS.

CC condensations and subsequence for a narbonolide PKS.

CC responsible for the production of many antiblotics including picromycin. The narbonolide PKS consists of a loading modile, six extender modules.

CC And two thiocaster domains. Four proteins make up the narbonolide PKS consists of a loading module with a strender modules and extender modules and PCAIN. PICAI includes the loading module of PICAII includes extender modules 3 and PCAIN includes extender module 6 and a type II thiocasterase domain. The second type II thiocasterase domain. The second type II thiocasterase domain. The second type II thiocasterase domain. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid pKOSO23-27. The recombinant form from from the recombinant cosmid pKOSO23-27. The recombinant DNA of the invention is used to cosmid pKOSO3-27. The recombinant DNA of the invention is used to cosmid pKOSO3-27. The recombinant phospide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by cother enzymes recombinantly expressed in the same hosts) to polyketide antibiolides or their intermediates. The antibiotics are useful in human contains and the decombinant processed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human contains the particularly hybrids in the particularly in the particular or their intermediates. The antibiotics are useful in human can be a converted to the particular or their encymes and the particular or 
                                                                                                                                                                                                                          /*tag= b
/product
/product= NR. tuberculosis cbhK homologous partial protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                                                                     /product= SAM_synthase
/note= "Partial S-adenosylmethionine synthase"
complement (3..692)
picromycin; antibiotic production; narbomycin; ds.
                                                                                     Location/Qualifiers
complement (694..1692)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 38; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0141908.
98US-0100880.
99US-0119139.
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                                             Streptomyces venezuelae
                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betlach MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-072618/06.
P-PSDB; Y67216, Y67217.
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1998;
28-AUG-1998;
22-SEP-1998;
08-FEB-1999;
                                                                                                                                                                                                                                                                                                             W09961599-A2
                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                            02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashley G,
                                                                                       Key
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Tang L;

Betlach M, McDaniel R,

ö Gaps ô 2; DB 21; Length 1693; 1.6; Indels 3.0%; Score 42.2; DB 21; 48.9%; Pred. No. 1.6; tive 0; Mismatches 118; Conservative Local Similarity Matches 113; Query Match

Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

797 gctgtactcgcctggggcagtgggccatcggctatgtgagctcagatggcagcatcctgc 856

> ð a

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857 agaccatccctgccaacaacccctgtcccaggtgctcctggagggacagaaggacggct 916
                                              911 AGACCTTCGGCACCCACAAGATCGAGACCGAGAAGATCGAGAACGCCATCGGCGAGGTCT
                                                                                                   917 tetacetetacecagatggaaagacecacaacecagacetgactgageteggeecaggeag
                                                                                                                                                                                                                                           791 AGACCGCCGCCTACGGCCACTTCGGCCGCGGAGCTGCCGGACTTCACCTGGG 741
                                                                                                                                                                                               977 aaccccagcagcatccacgtgtcagaggagcagctgcagctctactggg
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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds. S. venezuelae desosamine biosynthetic gene desv, SEQ ID NO:15. ВР. Z87290 standard; DNA; 1140 05-JUN-2000 (first entry) 287290; 287290/c

Streptomyces venezuelae ATCC15439

Location/Qualifiers 1..1140 /*tag= a /*tag= a /product= "DesV"

06-JAN-2000

WO200000620-A2.

99WO-US14398 25-JUN-1999; 98US-0105537 26-JUN-1998;

(MINU) UNIV MINNESOTA

ï 2hao Xue Y, Sherman DH, Liu H,

WPI; 2000-160679/14

P-PSDB; Y77185.

Desosamine and macrolide biosynthetic gene clusters, useful for, e .g. synthesis of methymycin and pikromycin -

Claim 3; Page 362; 438pp; English.

The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolides biosynthetic proteins are useful for synthesis of methymycin, pixromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or blomedical applications, to

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engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppresants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based bacteria, including multi-drug resistant preumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. Sequences 287286-287294 represent desosamine biosynthetic genes from Streptomyces venezuelae AICC 15439, which encode proteering y77181-Y77189.
                                                                                                                                                                                                                                                                                                                      1125 CCGCTCGGCCATTCGCGCACGGCGTCGATCACCCCCAGCGCCTGCGGGCGCCCCCAGGTG 1066
                                                                                                                                                                                                                                                                                            73 ctgcagcgcctagaagagcaatgcgtcgacccccggctgtccgtgagtccccttcgctg 132
                                                                                                                                                                                                                                                                                                                                                         252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 003; ketolide; dNDP glucose synthase; dehydratase; picromycin; narbomycin; antibiotic production; ds.
                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 gccggcggaggcgccccgggggtcccggcgctctggggactttctactcatctacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                               1005 TrccGGGGGGGCCTCGCCCGCGTAGGCGGGCGAGAGGTGCACGGGTACCGGGTAGTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= dNDP_glucose_synthase
/note= "glucose-1-phosphate thymidyl transferase"
1114..2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 agtgccaacgacgaggtcttccgggcgggctccagactcaggcgacagctggccaa 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     885 CACGGTGAAGAGGTGCCAGACCGGGTCGGTGTCGGGCGCGGGTCACCGGCAGGCCGA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig 003 from cosmid pKOS023-27 from Streptomyces venezuelae.
                                                                                                                                                                                                                                     Length 1140;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                     Sequence 1140 BP; 163 A; 472 C; 373 G; 132 T; 0 other;
                                                                                                                                                                                                                                   Score 41.6; DB 21;
Pred. No. 2.1;
                                                                                                                                                                                                                                                               0; Mismatches 159;
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104..982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                  2.98;
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                                                                                                                                                                                                                                                             Matches 137; Conservative
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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This is contig 003 from the recombinant cosmid pROS023-27 DNA sequence (see 256001) which contains a Streptomyces venezuelae DNA insert. The commination comparing frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to crecambinant DNA containing a coding sequence for a narbonolide PKS.

Polyketides are compounds synthasised from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the narbonolide PKS consists of a loading module, six extender modules of PCAIII includes extender modules and 4, produit includes extender module 5 and 4 produit includes extender module 5 and a type II thioesterase domain. The second type II thioesterase domain. The second type II thioesterase domain cosmid pKOS03-27. Narbonolide is desosaminylated in S. venezuelae to yield narbomyciú, the desosaminyl transferase enzyme is required for this convertson, and the desosaminyl blosynthetic genes are also found in cosmid pKOS03-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularily hypitals), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human continued the second pKOSO3-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3247 COGCICGGCCCATICGCGCACGGCGTCGATCACCCGCAGCGCCTGCGGGGCGCTCCAGGIG 3188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3127 ITCCGGCGCTGCCTCGCCCGCGTAGGCGGGCGAGAGGTGCACGGGTACCGGGTAGTGCGT 3068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3067 casegrarcarecasecesecercaacarecrecesecrecesecreseceseseseses 3008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 googgoggaggoggoccogggggtcocggoggctctgggggactttctactcatctacctg 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 egggacetgetgececegeaeagegeagetgettegagaggtggeeceatteteggeeggeeg
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                                                                                                                                                                                                                                                                                                                                   recombinant DNA encoding a domain of narbonolide polyketide
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                                                                                                                                                                                                                       R, Tang
                                                                                                                                                                                                                                                                                                                                                      synthase, for production of ketolide antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                       McDaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 41.6; Di
46.3%; Pred. No. 2.5;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 37-38; 98pp; English.
                                                                                                                                                                                                                     ×
                                                                                                                                                                                                                     Betlach
                                                                                                                                                                                                                                                             WPI; 2000-072618/06.
P-PSDB; Y67206, Y67214, Y67215.
                                                                                                                                                                           (KOSA-) KOSAN BIOSCIENCES INC
                     99WO-US11814.
                                                            98US-0087080.
98US-0141908.
                                                                                                         98US-0100880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                     Betlach MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 137; Conserv
                  27-MAY-1999;
                                                                                                                            08-FEB-1999;
                                                            28-MAY-1998;
28-AUG-1998;
                                                                                                         22-SEP-1998;
                                                                                                                                                                                                                  Ashley G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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3007 CACGGTGAAGAGGTGCCAGACCGGGTCGGTGTCGGGCGCGGTCACCGGCAGGCCGA 2952

/transl_except= (Pos:2874..2876, aa:Xaa) /note= "Xaa = Unknown"

WO9961599-A2

02'-DEC-1999

/*tag= c /product= PICCI

/product= d1 2124..3263

CDS

/*tag=

dNDP_glucose4_6_dehydratase

73 etyceagogoctagaagagcaatgogtogaccccoggotgtocgtgagtoccccttogotg 132

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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine of biologically active macrolides. The macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful to repare novel antibiotics and polyNdroxyalkanoate (PHA) arbomycin. The alternative termination of polyKetide synthesis may be useful to prepare novel antibiotics and polyNdroxyalkanoate (PHA) monomers. The compounds practoded by the recombinant host cells are useful as blopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fundalides a viral parasitic pathogens, or as crop protection agents (e.g., fundalides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster from Streptomyces venezuelae ATCC 15439.
                                                                                                                                                                                                    Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
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                                                                                                                                                               venezuelae desosamine biosynthetic gene cluster pikB, SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desosamine and macrolide biosynthetic gene clusters, useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12441 BP; 1704 A; 4294 C; 4686 G; 1757 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 281-287; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                  Streptomyces venezuelae AICC15439
                                     287284 standard; DNA; 12441 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xue Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US14398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105537
                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman DH,
                                                                                                                       05-JUN-2000
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RESULT
                   7284
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/product= "PixB gene cluster protein #6 (Y77208)"
/note= "No termination codon given in the specification"
/transl_except= (pos:8270..8275, aa:Yal)
/transl_except= (pos:8273..8275, aa:Thr)
/transl_except= (pos:8276..8278, aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoete monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product- "PikB gene cluster protein #1 (Y77204)"
/note- "No initiation codon given in the specification"
                                                                                                                                                                                   6397
6217
                                                                                                                      6278 ttccggcggtgcctcgcccgcgtaggcgggcgagaggtgcacgggtaccgggtagtgcgt 6337
                                                           cacggtgaagaggtgccagaccgggtcggtgtcgggcgcggtcaccggcaggccga 6453
6158 cogeteggeceattegegeaeggegtegateaceegeagegeetgegggegetecaggs
                                                                                          193 geoggeggaggeggeeceggggggteecggeggetetgggggaetttetaeteatetaectg
                                                                                                                                                         gocaatotggaggccaagagcaggcaggtggccgcgctgctgctccccgggggccgaagg
                                                                                                                                                                                    6338 gagggtgtcgatgccgcggggcgtcgaggtggctgcgcagctcgtcgcggcgctcggtgcg
                               cgggacetgetgeceegcacagegcagetgettegagaggtggeecatteteggegggeg
                                                                                                                                                                                                                  313 agtgecaaegaegagetetteegggegggeteeagaeteaggegaeagetggeeaa 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "PikB gene cluster protein #3 (Y77205)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "PikB gene cluster protein #5 (Y77207)"
complement (7942..8205)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "PikB gene cluster protein #2 (Y80998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "PikB gene cluster protein #4
/transl_except= (pos:6837..6841, aa:Gln)
7492..8205
                                                                                                                                                                                                                                                                                                                                                                                                                      S. venezuelae desosamine biosynthetic gene cluster pikB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "PikB gene cluster protein #7 complement (11271..12149)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces venezuelae ATCC15439
                                                                                                                                                                                                                                                                                                                           ВР
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/*tag= c
/product= "E
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Gaps

Query Match
2.9%; Score 41.6; DB 21; Length 12441;
Best Local Similarity 46.3%; Pred. No. 3.1;
Matches 137; Conservative 0; Mismatches 159; Indels 0;

193

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Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
            /*tag= k
/product= "PikB gene cluster protein #11 (Y77212)"
     'product= "PikB gene cluster protein #9 (Y77210)"
                                                                                                                                             WPI: 2000-160679/14.
P-PSDB; Y77204, Y77205, Y77206, Y77207, Y77207, Y77208, Y77209,
Y77210, Y77211, Y77212, Y80998, Y80999.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13613 BP; 1858 A; 4733 C; 5092 G; 1930 T; 0 other;
            complement (13706..15043)
                                                                                                                                                                                 synthesis of methymycin and pikromycin
                                                                                                                                                                                              Disclosure; Figure 32; 438pp; English
                                                                                                                                 Zhao L;
                                                                                                                                 Liu H, Xue Y,
                                                                                         99WO-US14398
                                                                                                     98US-0105537
                                                                                                                    (MINU ) UNIV MINNESOTA
                                                            WO200000620-A2
                                                                                        25-JUN-1999;
                                                                                                     26-JUN-1998;
                                                                                                                                 Sherman DH,
                                                                          06-JAN-2000
             CDS
                                  CDS
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comprising a descamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the error gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster acroades proteins which synthesise methymycin, playsynthetic gene cluster acroades proteins which synthesise methymycin, playsynthetic gene cluster acroades proteins which synthesise methymycin, playsophically active macrolides is are useful for macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, playsophic synthesis of methymycin, playsophic synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PRA) monomers. The compounds produced by the recombinant host cells are useful as bipolymers, e.g., in packaging or biomedical applications, to angineer PRA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, circular planmation, cholesterol-lowering agents or macrolide-based artibiotics which are active against a variety of organisms, e.g., chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other acceptratory pathogens, as well as virtal parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of protection agents or mercricides or insecticides) and other protection agents or protection agents or mercricides or insecticides) and other protection agents or protection agents or mercricides or insecticides) and other protection agents or mercricides or insecticides) and other process.
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invention relates to an isolated and purified nucleic acid
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                                                                                                                                 Gaps
                                                                                                                                                                   ctgcagcgcctagaagaagcaatgcgtcgaccccggctgtccgtgagtcccccttcgctg
                                                                                             Length 13613;
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                                                                                                                                 Indels
                                                                                           Score 41.6; DB 21;
Pred. No. 3.2;
0; Mismatches 159;
                                                                                             2.9%;
llarity 46.3%;
Conservative C
                                                                                                           Local Similarity
nes 137; Conserv
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Query Match

Matches

6845 73

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6905 egggeegateggeaggetgaggacetgeegegegaageteteggeeegegggagege 6964

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6965 ttccggcggtqcctcgcccgcgtaggcgggcgagaggtgcacgggtaccgggtagtgcgt 7024
geoggeggaggegecegggggteeeggegetetggggaetttetaeteatetaeetg 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An epitope of interacting protein (FIP protein) comprising anino acids 348-727 of the protein described in W96153, can be used to induce or prevent apoptosis in a cell. Specifically, decreasing the lavels of FIP348-727 prevents apoptosis. This is useful in cells which are dying prematurely, eg: Alzhelmer's disease, Acquired Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic lateral sclerosis (and other muscle wasting diseases), autoimmune diseases, and diseases where cells are infected with a pathogen (virus, bacteria; fungus, mycoplasm or protozoa). Increasing the levels of FIP 348-727 induces apoptosis which is useful in cells suffering from reoplastas, dysplasias, hyperplasias, or their symptoms. Purified and isolated FIP subgenomic polynucleotides are useful as primers to obtain more copies of the nucleotides, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                         FIP, FADD interacting protein; FADD; Fas-associated protein with a movel death domain; cell death; apoptosis; Alzbeimer's disease, Acquired Immune Deficiency Syddrome; AIDS; muscular dystrophy, amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasm;
                                                                                                                                                                                           7085 cacggtgaaguggtgccagaccgggtcggtgtcggggcgcggtcaccggcaggccga 7140
                                                                             gccaatctggkggccaagagcaggcaggtggccgcgctgctgctccccgggggccgaagg
                                                                                                                 gagggtgtcgatgccgcggggcgtcgaggtggctgcgcagctcgtcgcggcgctcggtgcg
                                                                                                                                                    313 agigecaaegaegaegaetetteegggeggegeteeagaeteaggegaeageiggeeaa 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New FADD (Fas-associated protein with a novel death domain)-Interacting Protein - useful for inducing or preventing apoptosis in a cell, to aid in controlling apoptosis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of human FADD (Fas-associated protein with a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protozoa; neoplasia; dysplasia; hyperplasia; ds
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''/label= Human_FADD_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
70..696
                                                                                                                                                                                                                                                                                                                                                                                                        Human FADD protein coding sequence.
                                                                                                                                                                                                                                                                                        X08910 standard; cDNA; 1582 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-095745/08.
P-PSDB; W96154.
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"Region encoding death domain"

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0
                                                                                                                                                                                                                                                                            216 getggageagaacgacetggageeegggeacacgageteetgegegagetgetegeete 275
                                                                                                                                                                                                                                                    81 cctagaagagaatgcgtcgacccccggctgtccgtgagtcccccttcgctgcgggacct 140
                                                                                                                                                                                                                                                                                                                       276 cetgeggegecacgacetgetgeggegegtegacgacttegaggegggggggggeggegg 335
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                         21 gtgggggggggacagtgggaagaggcccgggccctgggccgggcagtcaggatgctgcagog 80
probes that identify wild-type or mutant coding sequences. They are also useful for expressing FTP MRNA, proteins or fusion proteins, and in the generation of FIP antisense oligonucleotides and ribozymes. They are also useful in expression constructs and in gene delivery vehicles (optionally in combination with a condensing agent) that deliver FIP mRNA or oligonucleotides, FIP proteins (including variants), FIP-specific ribozymes or single-chain antibodies into eukaryotic cells. This is the human FADD protein gene. Human FIP protein binds to amino acids 1-110 of the human FADD protein given in W96154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note = "Encodes N-terminal half, inducing apoptosis but not binding Fas receptor"
                                                                                                                                                                                                                               156 gegegtggggaagegcaagetggagegegtgcagageggeetagaeetettetecatget
                                                                                                                                                                                                                                                                                                 Human; FADD; Fas-associating protein with novel death domain; apoptosis; Fas receptor; death domain; gene therapy; antibody; immunoassay; drug screening; diagnostic; AIDS; antiinflammatory; antitumour; cerebroprotective; neuroprotective; ss.
                                                                                                                                                                                  ;
0
                                                                                                                                                          Length 1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FADD (Fas-associating protein with novel death domain) gene.
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                             201 aggoggeceoggggggteeeggeggetetgggggaetttetaeteatet 247
                                                                                                                                                                                                                                                                                                                                                                    336 ggccgcgcctggggaagaagacctgtgtgcagcatttaacgtcatat 382
                                                                                                                           Sequence 1582 BP; 344 A; 433 C; 483 G; 322 T; 0 other;
                                                                                                                                                           Score 41.4; DB 20;
Pred. No. 2.4;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note="In-frame stop codon"
130.756
/*tag= c
/product= FADD protein
133.501
/*tag= d
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/note= "Clone 15 start point"
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/note= "Clone 8 start point"
460..660
/*tag= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            T39397 standard; cDNA; 1642 BP
                                                                                                                                                            Ouery Match 2.9%;
Best Local Similarity 48.9%;
Matches 111; Conservative
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The sequence encodes FADD (Fas-associating protein with novel death domain), which binds the cytoplasmic region of a Fas receptor, and modulates apoptorsis induced by activation of the receptor by ligand binding. The CDNA has been isolated using a yeast two-hybrid system which screens for proteins interacting with the Fas cytoplasmic domain. A GAL4-DNA-binding domain has been fined to the human Fas antigen cytoplasmic tail to form a bait plasmid, which is used with a prey plasmid, containing a human B-lymphocyte cDNA library fused to the GAL4-activation domain, to co-transform yeast cells.

COVELEDPING 10 brary using clone 15 as a probe. The CDNA has an human unbilical vein endothelial cell (HUVEC) library using clone 15 as a probe. The CDNA has an encoded protein contains a death domain, with interacts with the encoded protein contains a death domain, with interacts with the death domain of Fas. The DNA may be used in gene therapy, and the protein no a corresponding antibody may be used to screen for agents modulating FADD pathway cellular functions and Fas-associated apoptosis, for use in therapy of e.g. AIDS, inflammation, leukaemia, myocardial infarction, degenerative disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 cctagaagaagcaatgcgtcgacccccggctgtccgtgagtcccccttcgctgcgggacct 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             getggagcagaacgacetggageecegggcacaceggageteetgegegagetgetegeete 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FADD protein that binds to cytoplasmic region of Fas receptor identifying inhibitors of Fas-associated apoptosis useful for treating e.g. AIDS, leukaemia, stroke, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 ggccgcgcctggggaagaagacctgtgtgcagcatttaacgtcatat 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggoggococgggggtcocggcggctctggggactttctactcatct
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/note= "Reg
757..1642
/*tag= h
1636..1641
/*tag= i
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Best Local Similarity 48.9
Matches 111; Conservative
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P-PSDB; W03653.
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03-APR-1995;
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The present sequence encodes a human G-protein coupled receptor, designated Fishboy Enablets can be used to treat subjects in need of modulated Fishboy products can be used to treat subjects in to be treated include bacterial, protozoal, fungal and viral, particularly HIV-1 or HIV-2 infections, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina prostatic hypertrophy, migratine, vomitting, psychotic and neurological disorders and dyskinesias such as Huntington's disease or Tourette's
                                                                                                                                             Human; fishboy; G-protein coupled receptor; therapy; diagnosis; signal transduction; HIV; infection; pain; cancer; diabetes; obesity; anorexia; bulinha; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; stroke; osteoporosis; angina pectoris; myocadalal infarction; migraine; ulcer; allergy; benign prostatic hypertrophy; vomiting; dyskinesia; psychotic disorder; neurological disorder; Huntington's disease; Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new G-protein coupled receptor, Fishboy used to treat, e.g. benign
prostatic hypertrophy -
                                                                                                               Human fishboy G-protein coupled receptor encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1170 BP; 137 A; 409 C; 415 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       /product= "Fishboy"
/note= "a G-protein coupled receptor"
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                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP
                     ВЪ
239042/c
ID 239042 standard; cDNA; 1170
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98US-0133132.
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                                                                                                                                                                                                                                                                           Homo sapiens
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                                                  Z39042:
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The specification describes antisense oligonucleotides (X52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary visease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 AGGCGGCGGCCGGCCCGGGCTGCGCAGCCGAGCCCAGGAAGGGGCGGGTGACTGCG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 AGGCAGCGCTGCAGGCTGAGCAGGCCGGTGAGCACGCTGGCGTACATGCTGAGCGCG 396
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128 egetgegggacetgetgeceegcacagegeactgettegagaggtggeceattete-gg
                                                                                                                   TAGCAGCCGAGCATCAGCCCGAAAGGAAGCACGAAAGCGGTCAGAAGTCTCCAGGCTCAGG
                                                                                                                                                                                                                                                    cgggcggccggcggaggcggcccgggggggtcccggcggctctgggggactttctactcatc
                                                                                                                                                                                                                                                                                                                                                    TGGGCGCGCGCGTGGCGCCGCCGCCGCGCGCTGCCATACGCGGTCCTCCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacctggccautctggaggccaagagcaggcaggtggccgcgctgctgctccccgggggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgaaggagtgccaacgacgagtcttccgggcgggctccagactcaggcgacagctggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 CACACGTAGTACACCGCCTTGCAGCCCGCCTGGCCCAGCGGCCTGCCGG 342
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Length 1170; Indels

Score 41.2; DB 20; Pred. No. 2.5; 0; Mismatches 263;

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Conservative

2.98;

44.38;

Query Match Best Local Similarity Matches 210; Conserv

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67

815 TGGTAGGGGCCCCAGAGCCAAGCCAAGCAAGCACGATGGCGCTCACCAGCCGGCCCACC 756 ggatgctgcagcgcctagaagaagcaatgcgtcgaccccggctgtccgtgagtccccctt 127

tggcggtggcccgtggggggggcaagtgggaagaggcccgcgccctgggccgggcagtca

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regions and all segments of RNAs encoding proteins associated with one or more disease, conditions or mixtures. The antisense oligonucleotides may be derived from sequences X5572-74. These multiple target conjugated from sequences X55780-271, can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary vasconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, paracetic cancer, hepatocallular carcinoma, kidney cancer, melanoma, hepatic metastasize to the lungs, including breast and prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                            Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 104667 vgcggnnhnnnscggcgcgcccvggcccvgcgggnnhnnsgcggggcgcccvggcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 41.2; DB 20; Length :
; Pred. No. 5.6;
41; Mismatches 199; Indels
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Best Local Similarity 31.8%;
Matches 112; Conservative 4:
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T38913/c
ID T38913 standard; DNA; 880
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T30372 standard; cDNA; 1701
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                                  Conservative
                  Similarity
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                                  86;
Query Match
                  Best_Local
Matches 8
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                                                                                                                                                                 B2-bradykinin receptor gene exon 3 polymorphic region, allele BE3-R48
                                                                                                                                                                                                Tandem repeat polymorphism; B2 bradykinin receptor; diagnosis;
yocardial infarction; ocronary heart disease; dardomyopathy;
hypertension; genetically related vascular disease; sterility;
infertility; atopia; asthma; allergy; altered bronchial reactivity;
                                                                                                                                                                                                                                                                                                                                                                /*tag= a /note= "contains 48 tandem repeats with the consensus sequence TGGA(A)GGGCTAGAACC"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
117..841
/*tag= a
                                                                                                                                                                                                                                                                  acute; chronic; inflammation; ss.
                                                                                                                                    (first entry)
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Key repeat_region Homo sapiens

allele

15-MAY-1997

T38913;

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The present sequence represents allele BE3-R48 of the tandem-repeat polymorphic region of exon 3 of the B2-bradykinin receptor gene.

Two alleles have been identified, allele BE3-48R contains 48 tandem copies of repeat units with the consensus sequence rock(A)GGGCTAGAACC, while allele BE3-35R contains 35 copies.

The polymorphic sequences are useful for diagnosis (1.e. relating frequency of a polymorphism to disease occurrence) and/or treatment of myocardial infarction; coronary heart disease; cardiomyopathy; hypertension; genetically related vascular disease; sterility; infarction; asthma; allergy; altered bronchial reactivity, and acute or chronic inflammation. They can also be used to test potential drugs against such diseases and pharmaceuticals that contain angiotensin-converting enzyme inhibitors, kinin-receptor (ant)agonists
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/label- BE3-48R
/hote= "alternative allele BE3-35R contains 35
/hote= tandem repeats with the consensus sequence
TGGA(A)GGGCTAGAACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 40.4; DB 17; Length 880; 53.1%; Pred. No. 3.6; ive 0; Mismatches 76; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                             New polymorphic regions in the B2-bradykinin receptor gene diagnosis and treatment of bradykinin related diseases, e.g. myocardial infarction and allergy, and for drug assessment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 880 BP; 277 A; 170 C; 299 G; 134 T; 0 other;
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                                                                                                                  /rpt_type= TANDEM
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                                                                                                                                                         DE19518931-C1
                                                                                                                                                                                                                                    23-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 acgaectggageecegggeacacegagetectgegegagetgetegeteectgeggegee 361
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MORT-1; HF1; FAS/APOl receptor; FAS-R; tumour; cancer; HIV; mediator of receptor toxicity; gene therapy; ss.
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Pred. No. 4.9;
0; Mismatches 110; Indels
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                                                                             Location/Qualifiers
1..771
/*tag= a
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                                                                                                                                                                                                                                                                                                  (WEIN/) WEINWURZEL H.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 4; 72pp; English.
                                                                                                                                                                                                                                      951L-0114615.
941L-0112022.
951L-0112692.
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Best Local Similarity 49.1%;
Matches 106; Conservative (
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                                                                                                                                                                                                                                      16-JUL-1995;
15-DEC-1994;
19-FEB-1995;
                                               Homo sapiens
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ID	AF117646	AB028645	AF117647	HSCCBL	DMU87925	DMAJ3175	HSU26711	HSU26712	HSU26710	MMCCBL	CASNS1	03101004
		σ	Π	5	57	57	91	91	91	12	72	9
Query Match Length DB	1584	1575	1446	3090	2661	2529	3241	3354	3982	2808	17.5 2711	23766
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Location/Qualifiers
1. .1575
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42. .1466
                                                                                                                                                                                                                                                                                          /product="Cbl-c'
                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                    /gene="cbl-c"
42. .1466
//gene="cbl-c"
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Kim.Ms., Tezuka,T. and Yamamoto,T.

Kim.Ms., Tezuka,T. and Yamamoto,T.

Submitted (08-U0N-1999) to the DDBJ/EMBL/GenBank databases. Tadashi
Yamamoto, Institute of Medical Science, University of Tokyo,
Department of Oncology; Shirokanedal 4-6-1, Minato-ku, Tokyo
108-8639, Japan (E-mail:tyamamot@ims.u-tokyo.ac.jp,
Tel:+81-3-5449-5301, Fax:+81-3-5449-5413)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               1164 AICTACCAGIICTACGGICAGGCIACIGCIGAGGACICAGGGAACAGCAGTGACAGAAA
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                                                                                                                                                844 TACAICIICCGGCCCAGCIGIACIACICGGGGCAGIGGGCCAICGGCIAIGIAGAAC
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                                                       784 IICCICACCIAIGAGGICCAAGAGCGICIGCAGGCCIGCAGGGACAAGCCAGGCAGI
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Molecular cloning and characterization of a novel
cbl-c
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Homo sapiens
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT AB028645 LOCUS

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SOURCE

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REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

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THEREAGLISTER AGGGGGGGGGGGGGTDFLLIYLANIEAKSRQVAALLPPRG
RRSANDELFRAGSRLRRQLAKLAI IFSHMHAELHALFPGGKYGHWYGLITRAPAHITW
RESCOARCVLEWAEFESLLGFCHPVEPGCTALALFTTTIDLTCGGHYGIFEFDYFTRLP
OPWPTLIKNWOLLAVHIPGYMAFLYDEVOBRLQACRDKPGSYLYPDGKTHHPDLTTL
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SDSQTOPFCRCBIKGWRAVSIYQFYQQATABDSGNSSQOEGRELELGQYPLGARPFTPF
SDLPPRKRRNAQPRYRLLKGNSPAALGFQDDPAPA
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                                                                                                                                                                                                                                                                    /note="short form, alternatively spliced; cbl famil
protein; structurally related to the Sli-1 protein,
encoded by the cbl gene of Caenorhabditis elegans"
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                   Nau, M.N., Banerjee, P.,
                                                                                                                                                                                                /tissue_type="pancreatic adenocarcinoma"
1. .1446
                                                             Dept, Medicine
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Pred. No. 2.3e-191;
); Mismatches 2; In
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/db_xref="G1:4959423"
2 (bases 1 to 1446)
Keane, M. M., Ettenberg, S. A., Nau, M.N.,
Penninger, J. and Lipkowitz, S.
Direct Submission
Submitted (04-JAN-1999) Genetics Dept
Bethesda Naval Hospital, Bethesda, MD
Location/Qualifiers
:e
                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                 /map="19q13.2"
/cell_line="CF-PAC1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1446)
Keane,M.M., Ettenberg,S.A., Nau,M.M., Banerjee,P., Cuello,M.,
Penninger,J. and Lipkowitz,S.
Cbl.3: a new mammalian cbl family protein
Oncogene 18 (22), 3365-3375 (1999)
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Homo sapiens short CBL-3 protein (CBL-3) mRNA, alternatively
spliced isoform, complete cds.
AFI17647.1 GI:4959422
                          gatggcagcatcctgcagaccatccctgccaacaacccctgtcccaggtgctcctggag
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VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS

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Direct Submission
Submitted (02-0AN-1991) W.Y. Langdon, INSTITUTE OF MEDICAL
SUBMITTER (02-0AN-1991) W.Y. Langdon, INSTITUTE OF MEDICAL
VETERINARY SCIENE, IMVS, DIVISION OF HUMAN IMMUNOLOGY, BOX
VETERINARY SCIENE, ADELAIDE SA 5000, AUSTRALIA
2 (Dasses 1 to 3090)
Langdon, W.Y.

Eutheria;

Mammalia;

Vertebrata; e; Homo.

Eukaryota, Metazoa, Chordata, Ver Primates, Catarrhini, Hominidae; I 1 (bases 1 to 3090) Langdon,W.Y.

Direct Submission
Submitted (01-JAN-1991) Langdon W.Y., Institute of Medical und
Submitted (01-JAN-1991) Langdon W.Y., Institute of Medical und
Submitted (01-JAN-1991) Langdon W.Y., Institute of Medical und
Rundel Mali Post Office, Adelaide SA 5000, Australia
3 (bases 1 to 3090)
Blake, T.J., Shapiro, M., Morse, H.C. III. and Langdon, W.Y.
The sequences of the human and mouse c-cbl proto-oncogenes show
v-cbl was generated by a large truncation encompassing a
prolline rich domain and a leucine zipper-like motif
Oncogene 6 (4), 653-657 (1991)

4 (bases 1 to 3090)
Blake,T.J. and Langdon,W.Y.
A rearrangement of the c-cbl proto-oncogene in HUT78 I-lymphoma oells results in a truncated protein Oncogene 7 (4), 757-762 (1992)

1. 3090 /organism="Homo sapiens" /db_xref="taxon:9606"

/evidence=experimental

/gene="c-cbl" 1. .3090 149. .2869 /gene="c-cbl" /note="c-cbl protein" /codon_start=1

/gene="c-cbl" 149. .2869

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mRNA proto-oncogene.

HSCCBL LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT

oncogene cellular

Developmental Biology,

Biol. 17 (4), 2217-2225 (1997)

Mol. Celi. 97220014

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2 (bases 1 to 2661)
Daga,A., Meisner,H., Banerjee,U. and Czech,M.P.
Direct (Submission)
Submitted (30-JAN-1997) Molecular, Cell and Development:
Constity of California, Los Angeles, CA 90095, USA
Tocation/Qualifiers

ce //organism="Drosophila melanogaster"
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681 c 681 c 690 t 4 others

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  Score 329.2; DB 57; Length 2661; Pred. No. 3.7e-49; 0; Mismatches 333; Indels 3;
Query Match
23.2%;
Best Local Similarity 61.7%;
Matches 542; Conservative (
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iruit fly.

Drosophila melanogaster

Drosophila melanogaster

Drosophila melanogaster

BUKaryotta; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2661)

Meisner, H., Daga, A., Buxton J., Fernandez, B., Chawla, A.,

Banerjee, U. and Czech, M.P.

Interactions of Drosophila Cbl with epidermal growth factor

receptors and role of Cbl in R7 photoreceptor cell development

REFERENCE AUTHORS

TITLE

25-MAR-1997

cds

complete

mRNA,

mRNA D-cbl

GI:1842452

U87925.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

gecaacgacgactetteegggegggeteeagacteaggegacagetggecaagetggee Similarity 61.68; 11; Conservative Local Simi Query Match DEFINITION 316 376 556 1057 1357 1036 1417 1096 1153 1537 817 877 616 736 856 916 976 436 RESULT HSU26711 LOCUS Matches g D, B 8 Db g g ò 음 QΨ ŏ ŏ ð В ${}^{\circ}_{\lambda}$ g δ a ö g ğ ŏ ò ŏ ద ö g δ g ŏ /db_xref="SPTEMBL:046034"
/db_xref="SPTEMBL:046034"
/translation="MAIRGSOTRVGORIFPELLSKLHGAISEACVSQRLSTDKKTL
EKTANSLADKVVKLLOOPKMNLKNSPPFILDILPDTYQRLFLIYSKNBDQMHLHANBH
FNVFINNLMRKCKQAIKLFKEGKEKMFDENSHYRRNLIKLSLVFSHULSELKAIFPNG
FNVFINNLMRKCKQAIKLFKEGKEKMFDENSHYRRNLIKLSLVFSHULSELKAIFPNG
TCAPADPETTRADAADFWKRSTGNSTLIVPWK.RFRQEJNKVHPHISTGSTAMALKTIIDL
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GSYVFRLSCTRLGQWAIGYVTABGEILQTIPONKSLCQALLDGHREGFYLYPDGGAYN
PDLSSAVORSPEDHIYVTGROYELEQUYVDENGSTFQLCKICAENDKDIRLEDCGHLLCTPC
LISNWYDSEGGGGFRAERKGTEQIYVDAFDPRKQHNRNYUNGRQQQEEDDTEV"
661 C 564 9 647 t Submitted (22-DBC-1997) Hime G.R., Trescowthick Research Laboratories, Peter MacCallum Cancer Institute, Locked Bag 1, A Beckett St., Melbourne VIC, 3000 AUSTRALIA 2 (bases 1 to 2529) Hime, G.R., Dhungat, M.P., Ng, A. and Bowtell, D.D. Hime, G.R., Dhungat, M.P., Ng, A. and Bowtell, D.D. Interacts with the Drosophila EGF receptor in vivo, despite lacking C-terminal adaptor binding sites Oncogne 14 (22), 2709-2719 (1997) 1342 1035 1402 1095 1462 1152 28-DEC-1997 1283 TICIACITGIACCCAGAIGGCCAAGCGIACAAICCGGAICTGICGICGICGGITCAAAGI AGCACCITTCAGCTGTGCAAAATTTGTGCGGAGAAAGGAAAAAAATATCCGCATCGAGCCC tgogggcacctgctctgcagctgctgctggctgcctggca---gcactcggacagccag ttotacctetacccagatggaaagacccacaacccagacctgactgagctcggccaggca gaaccccagcagcgcatccacgtgtcagaggagcagctgcagctctactgggccatggac tecacatttgagetetgeagatetgtgetgagageaacaaggatgtgaagattgageeg 1463 IGTGGCCACTTGTTGTGCACTCCCTGCCTTACCTCCTGGCAAGTGGATTCCGAGGGACAG CCCACAGAGGACCACATAACCGTTACCCAAGAGCAATACGAACTATACTGTGAAATGGGC fruit fiy.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse

Bukaryota; Diptera; Brachycera; Muscomorpha; Ephydroidea;

Drosophilidae; Drosophila.

1 (bases 1 to 2529) Location/Qualifiers 1. .2529 7. granism="Drosophila melanogaster" /db_xref="taxon:7227" INV cbl gene. GCTGCCCTTCTGTCGGCCGAAATCAAGGCACCGA 1560 acctgccccttctgccgctgcgagatcaagggctggga 1190 /clone="pBluescript-1255" 328. 1674 /gene="cbl" 328. 1674 /codon_start=1 /protein_id="CAA11149.1" /db_xref="G1:2739273" DMAJ3175 2529 bp mRNA Drosophila melanogaster mRNA for AJ223175 GI:2739272 /chromosome="3" /dev_stage="embryonic" /map="666" cbl gene; proto-oncogene. 328. .1674 /gene="cbl" гđ Hime, G.R 657 RESULT 6
DMAJ3175
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS source SOURCE ORGANISM BASE COUNT ORIGIN AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL MEDLINE 916 1343 1036 1403 1096 gene 916 1523 REFERENCE CDS FEATURES q QΥ δŽ g ð g δ g ò g

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3241 bp mRNA PRI 30-SEP-1996 truncated form 1 lacking leucine zipper mRNA, complete
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697 GGCAAGGAGAAGATGTTCGACGAGAACTCCCACTACCGCCGCAATCTCACCAAGGTCAGĞ
                                                                            496 goooggigigigigoogggootgagitigagicootootgggoacoigcoocigig
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Human cbl-b
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7

Gaps

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Indels

Length 2529;

DB 57;

Score 327.6; DB 57; Pred. No. 7.2e-49; 0; Mismatches 334;

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HSU26712 3354 bp mRNA PRI 30-SEP-1996
Human cbl-b truncated form 2 lacking leucine zipper mRNA, complete
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( Dases, 1 to 3354)

Keane, M.N., Rivero-Lezcano, O.M., Mitchell, J.A., Robbins, K.C. and Lipkowitz, S.

Cloning and characterization of cbl-b: a SH3 binding protein with homology to the c-cbl proto-oncogene
Oncogene 10 (12), 2367-2377 (1995)
                                                                                                                                                                         979 AATTGATTTAACTTGCAATGATTACATTTCAGTTTTTGAATTTGATATTTTTACCAGGCT 1038
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    859 IGAATICIGGAGAAAGITITITIGGAGACAAAACIATICGIACCAIGGAAAGIAITCAGACA 918
                                             531 ectectggggaactgccaccetgtggaaccaggctgcacagccctggccttgcgcaccac 590
                                                                                      919 GTGCCTTCATGAGGTCCACCAGATTAGCTCTAGCCTGGAAGCAATGGCTCTAAAATCAAC 978
                                                                                                                                591 cattgacctcucctgoagcgggcacgtgtccatcttcgagttcgacgtcttcaccaggct
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/note="binds SH3 proteins; similar to c-cbl proto-oncogene
product, Swiss-Prot Accession Number P22681"
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TIDLCONDYLSYFEDIFTRLEOPWGSTLRNWKVFRQCLHEVHQISSSLEAMALKS
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ENEYFKIYIDSLMKKSKRAIRLFKEGKERMYEEQSQDRRNLTKLSLIFSHMLAEIKAI
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                                                                                Submitted (10-MAY-1995) Stan Lipkowitz, Navy Medical Oncology Branch, National Cancer Institute, Blg 8, Rm 5101, Bethesda Naval Hospital, Bethesda, MD 20889, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"alternative splice at nucleotide 2751 truncates protein before leucine zipper" 758 c 720 g 856 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="breast cancer cell line 2R75-1"
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/note="encodes nuclear localization signal"
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Pred. No. 3.4e-48;
); Mismatches 374; Indels
                                                                                                                                                                                                                                                                              2 (bases 1 to 3241)
Lipkowitz,S., Keane,M.M. and Mitchell,J.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="cbl-b truncated form 1"
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/note="encodes ring finger"
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/db_xref="GI:862409"
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ilarity 59.4%;
Conservative
GI:862408
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ENEYRIYIDSIAKKSKRAIRLEKEGKERWYEEQSORRNITKISLIFSHMAEIKAI
FPNGGFGONPRITKADAAEFWAKFFODTIVPWYVFRQCHEWHQISSSLEAMALKS
ITDLYCONDY ISYFEEDIFTHLEYDPWSSILRWNNFLAVTHPGYWAFITYDEVKARLOX
SIKFGSYIFRLSCTRLGQMAIGYVTGDGNILQTIPHNKPLFQALIDGSREGFYLYPDG
RYNPDLTGGLEBPTPHHIKYVDQYFELVERMSTFQLKCITCABNDSYNKIECGHLM
CISCLIAWQESDGQGPFCREGNEFITGNEFITYDFFDFADEGSSCCSILDFFGHLDD
DDDDREESLAMMNRLANVRKCTDRQNSPVTSPGSSPLAGRRKPQPDFLQIPHISLPPVP
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                                                                                                                                                                                                                                   /chromosome="3"
323. .263.
/note="similar to c-cbl proto-oncogene product, Swiss-Prot Accession Number P22681"
                                                                                                                                                                                                                                                                                                                         /product="cbl-b truncated form 2"
/protein_id="AAB09293.1"
/db_xref="G1:862411"
/db_xref="G1:862411"
/translation="WanSmNGRNPGGRGGNPRKGRILGIIDAIODAVGPPKQAAADRR
                                                                  Medical Oncology
5101, Bethesda Naval
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                                                                                                                                                                    /db_xref="taxon:9506"
/cell_line="breast cancer cell line ZR75-1"
/map="3q"
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/note="encodes nuclear localization signal"
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les 374; Indels
               2 (bases 1 to 3354)
Lipkowitz,S., Keane,M.M. and Mitchell,J.A.
Direct Submission
Submitted (lib.AM-1995) Stan Lipkowitz, Navy Med
Branch, National Cancer Institute, Blg 8, Rm 51C
Hospital, Bethesda, MD 20889, USA
Hospital, Location/Qualifiers

ce //organism="Homo Sapiens"
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/note="encodes ring finger"
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Pred. No. 3.3e
0; Mismatches
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al Similarity 59.4%;
548; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3982)

Keapa, M., Rivero-Lezcano, O.M., Mitchell, J.A., Robbins, K.C. and Lipkowitz, S.
Cloning and characterization of cbl-b; a SH3 binding protein with Oncogene:10 (12), 2367-2377 (1995)
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                                                                                              gctcctggaggacagaaggacggcttctacctctacccagatggaaagacccacaaccc
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1159 ACCCGGAAGCIAIATITICCGGITAAGTIGCACTCGATIGGGACAGIGGGCCATIGGCIA
                                                                  tytgageteagatggeageateetgeagaeeateeetgeeaaaaaeeeetgteeeaggt
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Lipkowitz, S., Keane, M.M. and Mitchell, J.A.
Direct Submission
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//db_xref="taxon:9606"
/cell_line="breast cancer cell
/map="3"/chromosome="3"
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Human cbl-b mRNA, complete cds.
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Blake,T.C: and Langdon,W.Y.
A rearrangement of the c-cbl proto-oncogene in HUT78 T-lymphoma
cells results in a truncated protein
Oncogene 7 (4), 757-762 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggccgtgagtatctaccagttccacggtcaggctactgctgaggactcagggaacagcag 1250
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1 (bases: 1 to 2808)
Langdon, W.Y.
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Submitted (01-JAN-1991) Langdon W.Y., Institute of Medical u Veterinary, Sciene, IMVS, Division of Human Immunology, Box Rundel Mail Post Office, Adelaide SA 5000, Australia 3 (bases 1 to 2808)
Blake, T.J., Shapiro, M., Morse, H.C. III. and Langdon, W.Y.
                                                                                                                                                                                                   1279 CCTGATTGATGGCAGCAAGGATTTTATCTTTATCCTGATGGGAGGAGTTATAATCC
                                                                                                                                                                                                                                                                                        agacctgactgactcggccaggcagaaccccagcgcatccacgtgtcagaggagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caacaaggatytgaagattgagccgtgcgggcacctgctctgcagctgctgcctggctgc
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/brotein_id="RaB09291.1"
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FPNGQFQGDNFRITKADAAEFWRKFFGDKTIVPWKVFRQCLHEVHQISSSLEAMALKS
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STREPSY IFRLESCTRLGGWAIGYYTGDGNILCT PHNRPLFOALLDGSREGFYLYPDG
RSYNPDLACEDPTHHONINYDEOVELYCENGSTFOLCKICAENDKOWIEPDG
RSYNPDLAGGESDGGGPFCCENGTEPI IVDPFPFRDEGSRCSIIDPFGWPMLDLD
DDDDREBSLAMNRLANTRCTDRGNSPYTSPGSSPLAGRRKPQPDFLGIPFLEBPPPP
PRLDLIQKGIVRSPCGSPTGSPKSSPCMVRKQDKPLRAPPPPLRDPPPPFRRPPIP
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VNGRHSRVGSDPVLMRKHRRHDLPLEGAKVFSNGHLGSEEYDVPPRLSPPPYTTLLP
SIKCTGPLANSLSEKTRDPVEEDDDEYKIPSSHPVSLNSQPSHCHNVKPPVRSCDNGH
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// Anote="interacts with SH3 proteins: similar to c-obl

// Anote="interacts with SH3 proteins: similar to c-obl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="encodes nuclear localization signal" 1439. 1558 /note="encodes ring finger" | 116. 3223 | 116. 3223 | 1043 t | 969 c 877 g 1043 t
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Pred. No. 3.1e-48;
0; Mismatches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.4%;
Matches 548; Conservative C
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CCAGATAIGTGCTGAGAA 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1011 TGTTACTGCGGATGGGAACATTCTGCAGACAATCCCACAACAATAAACCGCTCTTCCAAGC 1070
                                                                                        891 getectggagggaeagaaggaeggettetaeetetaeecagatggaaagaeeeaaeee
                                                                                                                                                                  1071 ACTGATTGATGGCTTCAGGGAAGGCTTCTATTTGTTTCCTGATGGACGAAATCAAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           getgeagetetactgggecatggactccacatttgagetetgcaagatetgtgetgagag
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                                                                                                                                                                                                                                                                                                                                                   1131 IGACCIGACAGGITTATGIGAACCAACTCCICAAGAICATATCAAAGIAAC-----
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691

471 GCAGACTATCAGCCTCTTCAAGGAGGGAAAAGGATGTATGAGGAGAATTCCCAGCC 530 291 ò g δ Q

650 actettecceggggcaaagtactgtggacacatgtaccagctcaccaaggccccgccca 411 g ğ

caccttctggagggaaagttgcggagcccggtgtgtgctgcctgggctgagtttgagtc 530

471

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GGCCCTGCATGAAGTGCATCCCATCAGTTCTGGGCTGGAGGCCATGGCTCTGAAGTCCAC 770 CGAATTTTGGAGAAAAGCTTTTGGTGAAAAGACGATAGTCCCGTGGAAGAGCTTTCGACA cetectggggcacetgccaccetgtggaaccaggetgcacagccetggccttgcgcaccac 651 531 711 a gg $\overset{\circ}{\alpha}$

710 591 cattgacctccacctgcagcgggcacgtgtccatcttcgagttcgacgtcttcaccaggct 771 TATTGATCTGACCTGCAATGATTATATTTCTGTCTTTGAATTTGATATTTTACACGCT ΟŽ g QY Db

890 ctttcagccatggccaacactcctcaagaactggcagctcctggcagtcaaccaccagg 831 GITTCAGCCCTGGTCCTCTTTGCTCAGAATTGGAACAGCCTTGCTGAACTCACCCTGG 711 ctacatggcottcctcacctatgatgaggtccaagagcgtctgcagggcctgcagggacaa 651

ŏ g

Qγ g

tgtgagctcagatggcagcatcctgcagaccatccctgccaacaacccctgtcccaggt

831

890

braft entry and computer-readable sequence for [1] kindly submitted by W.Y.Langdon, 02-MAR-1989. Cas NS-1 is an acutelly transforming murine retrovirus that induces pre-be and pro-B cell lymphomas. It was generated from the ecotropic Cas-Br-W virus by sequential recombinations with endogenous retroviral sequences and a ceilular oncogene. The position of the oncogene junction was determined be in the gag gene for p10 at a position that removed the termined to be in the gag gene for p10 at a position that removed the termined be responsible for fibroblast and pre-B cell transformation. The authors call this oncogene v-cbl for Casitas B-lineage lymphoma. 1 (bases 1 to 2711)
Library M. Y., Hartley, J.W., Klinken, S.P., Ruscetti, S.K. and Morse, H.C. III.
V-Cbl, an oncogene from a dual-recombinant murine retrovirus that induces early B-lineage lymphomas
Proc. Natl. Acad. Sci. U.S.A. 86, 1168-1172 (1989)
89145204 CASNS1 CAT11 bp DNA VRL 02-AUG-1993 Mouse Cas NS-1 retrovirus gag-onc fusion protein (v-cbl) gene, J04169 J04169.1. GI:323269 J04169.1. GI:323269 J04169.1. GI:323269 J04169.1. GI:323269 J04169.1. GII:323269 J0416.1. GIII Infected With Cars Br-M virus. J0416.1. GIII Murine leukemia virus. Viruses, Retroid Viruses, Retroviridae, Mammalian type Cretroviruses; I-Mammalian type Cretrovir /organism="Cas NS-1 murine leukemia virus" //db_xref="taxon:11793" <1. .1609 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL MEDLINE COMMENT REFERENCE AUTHORS PEATURES TITLE RESULT CASNS1

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Consensus quality: 22899 bases at least Q40
Consensus quality: 238912 bases at least Q30
Consensus quality: 238312 bases at least Q30
Consensus quality: 238312 bases at least Q30
Consensus quality: 238312 bases at least Q30
Estimated insert size: 240000; agarose-fp estimation
Quality coverage: 7.5 in Q20 bases; sum-of-configs estimation
Quality coverage: 7.5 in Q20 bases; sum-of-configs estimation
Quality coverage: 7.5 in Q20 bases; sum-of-configs
**are represented as runs of N. The order of the pieces
is balieved to be corred N. The order of the pieces
of the gaps between them are based on estimates that have
provided by the submitter.

This sequence will be replaced

**public finished sequence as soon as it is available and
the accession number will be preserved.

This sequence will be replaced

**public finished sequence as soon as it is available and
the decasion number will be preserved.

1308: contig of 14982 bp in length
1409 16390: contig of 14982 bp in length
14101 16490: gap of unknown length
14101 16490: gap of unknown length
14101 16490: gap of unknown length
14101 1650: contig of 5599 bp in length
14101 1650: gap of unknown length
1509: 11055: gap of unknown length
1500: 11055: gap of unknown length
1500: 11055: gap of unknown length
1500: 12111 contig of 1409 bp in length
1500: 12111 contig of 1409 bp in length
1500: 12111 contig of 1409 bp in length
                                                                                                                                   Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence Version replaced 91:8810377.
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58023 a 59212 c 60636 g 58282 t 1500 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 18980 bp in length
gap of unknown length
contig of 3359 bp in length.
                                                                                                                                                                                                                                                                                                                                                                         Project Information
Center Project Name: 1749735
Center clone name: RPCI-23_33H23
                                                                                                                                                                                                                                                                                                                            Web site http://www.jgi.doe.gov
                                                                                                                                                                                                                                              -----Genome Center
Center: Joint Genome Institute
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                                                        Unpublished
2 (bases 1 to 237653)
DOE Joint Genome Institute.
     DOE Joint, Genome Institute
Sequencing of Mouse
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                                                                                                                                                                                                                                                                                                Center Code: JGI
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     AUTHORS
TITLE
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                                                                                 REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                    COMMENT
GLEAMALKSTIDLICNDYISVFEFDIFTRLEQPWSSLLRNWNSLAVTHPGYMAFLTYD
BYKARLQKFIHKPGSYIFRLSCTRLGGWAIGYVTADGNILQTIPHNKPLFQALIDGFR
EGFYLFPDGRNQNPDLTGLCEPTPHFS"
752 a 688 c 583 t
1 bp upstream of XbaI site.
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Mus musculus clone RP23-33H23, WORKING DRAFT SEQUENCE, 16 ordered
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 237653)
                                                                                                                                                                                                                                                                                                                                                                                                                                            967 TAGGGGAAACCTGACCAAATTATCCCTGATCTTCAGGCACATGCTGGCAGAACTGAAAGG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 CATCTITCCGAGCGGACTCTTCCAAGGAGACACTTTCCGGATTACTAAAGCTGATGCTGC 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1207 TATTGATCTGACCTGCAATGATTATATTTCTGTCTTTGAATTTGATATTTTACACGGCT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1147 GGCCCTGCATGAAGTGCATCCCATCAGTTCTGGGCTGGAGGCCATGGCTCTGAAGTCCAC 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1387 ACCTGGCAGTTACATCTTTCGGCTGAGCTGTACTCGTTTGGGTCAGTGGGCTATTGGGTA 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1447 IGTTACTGCCGATGGGAACATTCTGCAGACAATCCCACACAATAAACCGCTCTTCCAAGC 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  caggogacagotggcoaagotggcoatcatcttcagcoacatgoacgoagagotgcacgo
                                                                                                                                                                                                                                                                                                                                             907 GCAGACTATCAGCCTCTTCAAGGAGGGAAAGGAAGGATGTATGAGGAGAATTCCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771 gccaggcaggtacatcttccggcccagctgtactcgcctggggcagtgggccatcggcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 actottococggggcaaagtactgtggacacatgtaccagotcaccaaggcocccgccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1087 CGAATITIGGAGAAAAGCITITIGGIGAAAAGACGATAGICCCGIGGAAGAGCITITCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 cctcctgggcacctgccaccctgtggaaccaggctgcacagccctggccttgcgcaccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cattgacctcacctgcagcgggcacgtgtccatcttcgagttcgacgtcttcaccaggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 ctttcagccatggccaacactcctcaagaactggcagctcctggcagtcaaccaccagg
                                                                                                                                                                                      17.5%; Score 248.2; DB 72; Length 2711; 59.9%; Pred. No. 8.1e-35; Live 0; Mismatches 278; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1567 TGACCTGACAGGTTTATGTGAACCAACTCCTCA 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 agacctgactgagctcggccaggcagaacccca 983
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HTG: HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                   Query Match
Best Local Similarity 59.9
Matches 415; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
Mus musculus
                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471
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KEYWORDS
SOURCE
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CEDNASLI1 2230 bp DNA INV 15-NOV-1995

C.elegans DNA for sli-1 gene.

NX 839223

X89223.1 GI:895766

Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans.

ISM Caenorhabditis elegans.

ELKaryota; Metazoa; Nematoda; Secernentea; Rhabditida;

ELKaryota; Metazoa; Nematoda; Rhabditidac; Peloderinae; Caenorhabditis.

ELKaryota; Metazoa; Nematoda; Rhabditidac; Peloderinae; Caenorhabditis.

ELKaryota; Metazoa; Nematoda; Rhabditidac; Peloderinae; Caenorhabditis.

S. Yoon, C. H., Lee, J., Ongeward, G. D. and Sternberg, P. W.

Similarity of Sli-1, a regulator of vulval development in C.

Similarity of Sli-1, a regulator of vulval development in C.

Solence 269 (5227), 1102-1105 (1995)
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Length 237653;
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Direct Submission
Submitted (28-10N-1995) C.H. Yoon, CALIFORNIA INSTITUTE (Submitted (28-10N-1995) C.H. Yoon, CALIFORNIA INSTITUTE (TECHNOLOGY, Div. of Biology, Pasadena, CA91125, USA Location/Qualifiers
                                 'n
Score 214.2; DB 60; Length
Pred. No. 1.7e-29;
0; Mismatches 88; Indels
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.Coganism="Caenorhabditis elegans"
/strain="N2"
.db_xref="taxon:6239"
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/clone_lib="Barstead"
/map="-20 to -24.50 mm
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/gene="sli-1"
Query Match
Best Local Similarity 75.5%;
Matches 280; Conservative
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/ db_xref="SPTERMEL:019019"

/ translation="MGSINTIFHRIPEVNGTGNNARFVPSTNNSTEALTLSPRAVES

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DTWIHLINIFTQNNDILORDOYLK FILESMINKCEXIKLETKRINTOPWSTFFTALE

KHHGSTGSTGKREADEKATIDLSGDDFISNFERDVFTRYPRFYRNIVPWSTFFTALE

KHGSTGSTGKREADEKATIDLSGDDFISNFERDVFTRYPRENTRYNITARPG

VCAPLTYDBVKRILERLTRKGSYLFILSCTRPGQNALGYVAPDGKIYOTIPQNKSLI

QALHEGHKSGYTYPWGROINLSKIMDVPQADRYQYTSEQTINTUIDRFKPTPV

EIEKARWVAAREKKLISLVPDVPPRTYVSQCSQSLLHDASNSIPSVDELPLVPPPLPP

KALGTLDTLMSSGTSSSYVNIKKELENVETSGFALAQVVNRQRAPSIQAPPLPPRLSAS

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14.0%; Score 199.4; DB 33;
Best Local Similarity 53.5%; Pred. No. 3.8e-26;
Matches 466; Conservative 0; Mismatches 396;
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e2 154

/codon_start=1 /protein_id="CAA61507.1" FG 20-MAY-2000 *** SEQUENCING IN

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Drosophila melanogaster

Eukaryotta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryotta; Meoptera; Endopterygotta; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila

SE Muscomorpha; Ephydroidea; Drosophilidae; Drosophila

Burkett, Burch, Balley, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,

Burkett, Burrows, J., Carter, M., Cherko, J., Chen, Z., Cox, C.,

David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

Forcum-Transey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, T., Guevara, W., Harris, K., Hernandez, C., Ferraguto, D., Hogues, M., Holloway, C., Hosak, H., Jackson, L., Jackson, J., Jay, Y., Gorrell, J., H., Jackson, J., Jay, Y., Kowar, C., Leal, B., Litz, I., Liu, W., Logan, C., Lozado, R., Li, J., Liu, W., Logan, R., Nguyen, S., Nash, S., Nash, S., Nash, S., Parton, B., Parton, B., Samuel, S., Shan, H., Simon, M., Samuel, S., Say, J., Scherer, S., Shan, H., Simon, M., Samuel, S., Shan, H., Simon, M., Samuel, S., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I. R., Williamson, A., Walbah, R., Walligh, R., Went, J., Williamson, D., and Gibhs, R.
                                                                                    Drosophila melanogaster clone RPC198-315, PROGRES ***, 75 unordered pieces. ACC10033 ACC2749 GI:7958624
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Unpublished
2 (bases 1 to 12926)
Worley, K.C.
Direct Submission
                                                                  129226 bp
                                                                                                                                                                                         HTG; HTGS_PHASE1. fruit fly.
                                                                     AC010033
                                                                  LOCUS
DEFINITION
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AUTHORS
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                       RESULT 1
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ACO14994.1 GI:6436341
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FINIT FIGS_PHASE2.

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FINIT FIGS_PHASE2.

ENARYORIS MEADORS ATTHOROOGS; TRACHERATS; BEACHYCERS; PLOSOPHILE BEACHYCERS; BUDGECT SUBMITTED (16 NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA 3040HILE SEQUENCE e-mail to fly@celera.com.
** NOTE: This is a 'working draft' sequence -mail to fly@celera.com.
** NOTE: This is a 'working draft' sequence.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
                                                                                                                                                                                                                                                                 HTG 16-NOV-1999
IN PROGRESS ***, in ordered
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                         506 tgctgccctgggctgagtttgagtccctcctgggcacctgccaccctgtggaaccaggct 565
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/db_xref="taxon:7227"
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Pred. No. 5.3e-23;
0; Mismatches 138
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Contact: has a harmonia contact; has a harmonia contact name; program special contact name; program; prog
Submitted (11-5EP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 20, 2000 this sequence version replaced gi:6996835 gi:6996719.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Search completed: December 7, 2000, 13:48:28 Job time: 28040 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Search time 79.91 Seconds (without alignments) 2927.917 Million cell updates/sec 7, 2000, 06:02:31 December Run on:

Title: Perfect score:

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IDENTITY_NUC Gapext 1.0 Scoring table:

262060 seqs, 75620496 residues Searched:

524120 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

ULT 1 -US93-06251-7 equence 7, Application PC/TUS9306251	APPLICANT: Wirkstrom, Eric and Rife, Jason P. TILLE OF INVENTION: Trivalent Synthesis of Oligonuclectides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SOURCES: 93	CORRESPONDENCE ADDRESS: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: NY COUNTRY: USA ZIP: 11530	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Eloppy disk COMPUTER: Eloppy disk COMPUTER: Eloppy disk COMPUTER: Parentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/06251 APPLICATION NUMBER: PCT/US93/06251 FILING DATE: 19930630 CLASSIFTCATION: ATTORNEY/ABCHT. INCOMMATION: NAME: Digiglio, Frank S. REGISTRATION NUMBER: 8886 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMAT	Query Match 22.0%; Score 340; DB 6; Length 3090; Best Local Similarity 62.2%; Pred. No. 1.8e-59; Marches 537. Conservative 0. Mismatches 325. Indels 0. Gars 0.
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Score 46.4; DB 5;
Pred. No. 0.066;
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TYPE: DNA
CRGANISM: Streptomyces venezuelae
US-09-320-878-22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 3292
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OKSOLIT 48

OKSOLIT 59

Sequence 22, Application US/09320878A

Fatent No. 6117669

FAPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Melanie C.

EARLIER TELING DATE: 1998-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-08

EARLIER FILING DATE: 1998-05-28

NUMBER OF SEQ ID NOS: 34
        INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE SRENCE: 300622002120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 AGACCGCCGTACGCCCACTTCGCCGCGAGCTGCCGGACTTCACCTGGG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.2; DB 5; Length 1 Pred. No. 0.37; 0; Mismatches 118; Indels
                                  FILE STRUCKES 3006, 2002 DELANGE STRUCKES OF STRUCKES APPLICATION UNDERS: CIP OF 09/073,538 EARLIER FILING DATE: 1998-05-06 STRUCKES APPLICATION UNDERS: CIP OF 08/846,247 EARLIER APPLICATION UNDERS: 60/119,139 SARIER FILING DATE: 1999-02-08 SARIER APPLICATION UNDERS: 60/100,880 SARIER PARIER SARIER SAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces venezuelae US-09-320-878-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%;
Best Local Similarity 48.9%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
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3128 TICCGGCGCTGCCCCCCCCGCTAGGCGGCGAGAGGTGCACGGGTACCGGGTAGTGCGT 3069
                                                                                                                                                                               3248 CCGCTCGGCCCATTCGCGCACGGCGTCGATCACCCGCAGCGCCTGCGGGCGCTCCAGGTG 3189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 cagogcagetgettegagaggtggeecatteteggeeggeggeggeggaggeggeeceg 223
                                                                                                                                                                                                                                                                                                                                                           205 geoggeggaggegeecegggggteeeggeggetetgggggaetttetaeteatetaeetg 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 aginggaaagagcoogogcootgggoogggoagtoaggaigcigoagogootagaagagc 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 agogcaagotygagogogtgcagagoggcotagacctcttctccatgctgctggagoaga 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 aatgogtogaccocoggotgtocgtgagtococttogotgogggacotgotgocogoa 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                      85 ctgcagcgcctagaagagcaatgcgtcgacccccggctgtccgtgagtcccccttcgctg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 gecaatetggaggecaagageaggeaggtggeegeetgetgeeteeeeggggeegaagg 324
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3008 caceercaasasersceasaccesercesrercesecesesces acceseases
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                                                                                                                                                                                                                                        325 agigecaacgaegagetetteegggegggeteeagaeteaggegaeagetggeeaa 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-357-072-1
Sequence 1, Application US/09357072
Patent No. 6015712
GENERAL INFORMATION:
APPLICANT: Bretdt F. Monia
APPLICANT: Hong Chang
APPLICANT: Hong Laker
APPLICANT: Hong Laker
TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
TITLE OF INVENTION: ANTISENSE
CURRENT APPLICATION NUMBER: US/09/357,072
CURRENT FILLING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 87
Length 3292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match . : 2.6%; Score 40; DB 5; Length 1701; Best Local Similarity 49.1%; Pred. No. 1.2; Matches 106; Conservative 0; Mismatches 110; Indels
Score 41.6; DB 5; Length 3 Pred. No. 0.61; 0; Mismatches 159; Indels
Query Match 2.7%;
Best Local Similarity 46.3%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (145)..(771)
US-09-357-072-1
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LENGTH: 1701
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MODULATORS OF THE FUNCTION OF FAS RECEPTORS AND OTHER PROTEINS
                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS REC
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIOM IYPE: Floppy disk
COMPUTER: ISM COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
                                                                                                                                                                     422 GGGAAGAAGACCTGTGTGCACATTTAACGTCATAT 457
                                                                                                                                               224 ggggteceggöggetetggggaetttetaeteatet 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DAWLE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 16-JUL-1995
PRIOR APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR 1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEDENTH: 1701 Dase pairs
                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9610521
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.1%;
Matches 106; Conservative (
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EDNESS: single
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STRANDEDNESS:
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PCT-US96-10521-1
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                                                                                                    APPLICANT: WEDA RESEARCH AND DEVELOPMENT CO. LTD.
APPLICANT: WEDANGEL, Henry
APPLICANT: WEIMWINSEL, Henry
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: WARROLOWERV, Bugene
APPLICANT: MATT, IGOR
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNY ****
STRFFT
STRFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 6; Length 170 Pred. No. 1.2; 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16542
    224 ggggtcccggcggctctgggggactttctactcatct 259
                              422 gggaagaagacctgtgtgcagcatttaacgtcatat 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112022
FILING DATE: 15-DEC-1994
PRIOR APPLICATION NUMBER: IL 112692
FILING DATE: 19-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114615
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114615
ATTONNEY, AGGNT INFORMATION:
NAME: BROWDY, ROGET I.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 35,618
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C. : United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6%;
Best Local Similarity 49.1%;
Matches 106; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Sevent
CITY: Washington
STATE: D.C.
COUNTRY: United St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS;
; LOCATION: 1..7
PCT-US95-16542-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                    RESULT 6
PCT-US95-16542-1
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44 agtgggaagagcccgcgccctgggccgggcagtcaggatgctgcagcgcctagaagagc 103
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                                                                                                                                                                                                                                                             104 aatgogtogaccccoggetgtccgtgagtccccttcgctgcgggacctgctgcccgca,163
                                                                                                                                                                                                                                                                                                                          302 ACGACCTGGAGCCCGGGCACACCGAGCTCCTGCGCGAGCTGCTCGCCTCCCTGCGGGGGCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
Score 40; DB 5; Length 1701;
Pred. No. 1.2;
0; Mismatches 110; Indels
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104 aatgegtegaeeeeeggetgteegtgagteeeettegetgegggaeetgeeegga 163

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 cettegetgeggacetgetgeceegeacagegeacagetgettegagaggtggeceattet 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 getetggeggtggeeeegtgggggegacagtgggaagaggeeegegeeetgggeegggea 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4692;
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                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TRACESO for Windows
SOFTWARE: FractSO for Windows Version 2.0b
CURRENT APPLICATION DATA: US/08/916,917
FILING DATE: 15-406-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-7UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                  224 ggggtcccggcggctctggggactttctactcatct 259
                                                                                    422 GGGAAGAAGACCIGIGIGCAGCAITTAACGICATAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 38.4; Local Similarity 50.9%; Pred. No. 3.0 Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CIII: New York
                                                                                                                                                                                                                                                                          08-08-916-917-1/c
; Sequence 1, Application US/08916917
; Patent No. 5856132
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TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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US-08-916-917-1
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QΣ ε.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.4; DB 3; Length 4 Pred. No. 3.6; O; Mismatches 111; Indels
Sequence 1, Application US/08972631

Patent No. 5856133

GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION:
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' K1
NUMBER OF SEQUENCES: 10
CORRESONEDER ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/672,211
APPLICATION NUMBER: 27-UN-1996
ATTORNEY/ABENT INFORMATION:
RAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REPRENDENCYET YOUNGER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,854.3660
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08972629
Patent No. 5859201
GENERAL INFORMATION:
APPLICANT: Stephens, Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1) 2.5%;
ilarity 50.9%;
Conservative
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Best Local Similarity
Matches 116; Conservat
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                                                                                                                                                                                                                                                                               CITY: Menlo Park
STATE: Californi
COUNTRY: USA
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US-08-972-629-1/c
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2730 Sand Hill Road
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                              CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-972-630-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 getetggeggtggeecegtgggggggaeagtgggaagaggeecgegegeecgggee 75
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Pred. No. 3.6;
0; Mismatches 111; Indels
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMAA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08972630
Patent No. 5869271
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TILLE OF INVENTION: G-BETA-GAMMA REGULATED
'TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,629
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-7UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,854-3560)
                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%;
Best Local Similarity 50.9%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-972-629-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-972-630-1/c
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1833 GCTTGGGCTGGGGCAGCGGAG-CCCTGGGCCCGGGAACGGGGCAGGGTG 1775
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US-08-672-211-1/C
US-08-672-211-1/C
Sequence 1, Application US/08672211
Sequence 1, Application US/0867211
Seq
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                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/972,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.5%; Score 38.4; DB 3;
Best Local Similarity 50.9%; Pred. No. 3.6;
Matches 116; Conservative 0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PLING DATE: 27-JUN-1996
ATTORNEY/AGENT ENFORMATION:
NAME: Halluli, Albert P.
REJESTRATION NUMBER: 25,277
REFERENCE / DOCKET NUMBER: 25,277
RELECOMMUNICATION INVERENT P.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                              ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)854-3694
INFORMATION FOR SEG ID NO: 1
SEGUIENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
California
USA
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STRANDEDNESS
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US-08-680-506-5/c
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US-09-225-170-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1833 GCTTGGGCTGGGGCAGCGGGAG-CCCTGGCCCCGGACGGGGCAGGGTCGGGCTG 1775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 cettegetgeggaeetgetgeeeggeaeaggegeaggetgettegagaggtggeeeattet 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 4692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38.4; DB 3; Length 46 Pred. No. 3.6; 0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1654 ATCCTGTTGAACTTCTGCCGGGGCGGGGGGGCCCCGGGGCTCGTGG 1607
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Fatent No. 6017763
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Brasslmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
ITILE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/^-
FILLING DATE:
                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
RECISTRATION NUMBER: 25,277
REFERENCE/COCKET NUMBER: 8549:
TELECOMMUNICATION: (415)844-360
TELEFAX: (415)844-360
INFORMATION: POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.5%;
Best Local Similarity 50.9%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: CDNA
US-08-672-211-1
                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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50.2%; Pred. No. 2.6;
tive 0; Mismatches 118;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
RABGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 849-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFHONE: 650-493-5556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
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Best Local Similarity 50.2
Matches 120; Conservative
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CORGANISM: Gallus gallus
US-08-680-506-5
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                       270 GCGGAGGCGGTGCAGCTCGGCGAGCGGGATTTGCCCGGCCGTGGGGGTAGCGGGT 211
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                                                                       294 ggccgcctgctgcctccccggggccgaaggagtgccaacgacgagctcttccggggcgg 352
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                                                                                                                                                                                             Sequence 8, Application US/08680506C
Patent No. 6008013
GENERAL INFORMATION:
APPLICANT: REPROBATION:
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REPERENCE: 176/60091
CURRENT PILING DATE: 1996-07-08
EARLIER FILING DATE: 1996-07-08
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-8
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US-08-680-506-8/c
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Search completed: December 7, 2000, 13:40:01 Job time: 27450 sec

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Search time 152.48 Seconds (without alignments) 3811.321 Million cell updates/sec
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// SIDSS/gcgdata/geneseq_/geneseqn_NA1980.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1981.DAT:

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// SIDSS/gcgdata/geneseq_/geneseqn_NA1982.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1983.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1985.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1986.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1980.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1980.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1991.DAT:

// SIDSS/gcgdata/geneseq_/geneseqn_NA1992.DAT:

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                - nucleic search, using sw model
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1547
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater then or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human adenosine Al Contig 004 from co S. venezuelae deso Contig 003 from co S. venezuelae deso S. venezuelae deso Human FADD protein FADD (Fas-associat Nucleotide sequenc Gene encoding a su Human adenosine Al Mycobacterium smeg Description A10594 X53491 V58939 X53491 Z56005 Z87290 X89079 101111100010 DB 22.0 3090 3.1 10732 3.0 9965 2.8 114955 2.7 1693 2.7 1693 2.7 12441 2.7 13613 2.7 13613 2.7 1642 Length Query Score Result 0000

encodi n fishb radykin n enzym n adenc -1 cDNA	Human FADD DNA. H Amycolatopsis medi MORTI isoform MORT Cartilage derived Porcine betal-adre Rianodin receptor	acet calc inin e se enco	ne phosphoi ne G-protei 101 regulati s domesticu s domesticu s domesticu	allus equenc cuse N n5099- equenc H muta
X81941 Z39042 T38913 X55273 A34721 T30372	71010	0 0 1 0 4 10 6	44000000 0000000	V19860 V19860 X087820 Q68194 Q25975
20 120 137 187	121 121 121 121	20120	0000000	3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
2644 1170 880 6225 1701	1701 53789 627 1308 2170 15672	73 363 643 753 174 291	446992 466992 13447 46887	2002 2002 2002 33150 53302 153302
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ALIGNMENTS

X89079 standard; DNA; 3090 BP

RESULT X89079

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                                 The invention relates to a protein tyrosine kinase substrate LAT (linker for activation of T cells) protein. Modulation of interaction between LAT and the T-cell receptor (TCN) affects the TCR signalling pathway. LAT is a substrate for tyrosine Kinases and becomes phosphorylated after TCR engagement, resulting in recruitment of other signalling molecules. LAT is used to identify and test (ant)agonists of tyrosine Kinase signalling pathways, i.e. modulation of interaction between tyrosine kinase substrates and intracellular ligands or between these ligands and other members of the pathway including identification of downstream signalling proteins, particularly in immune system cells. These modulators are potentially useful as drugs and diagnostic agents, particularly in immune system cells. These modulators are potentially useful as drugs and diagnostic agents, particularly for diseases that involve undesirable cell proliferation, differentiation, growth or T cell anergy, e.g. neoplasia, inflammation, differentiation, and is assess, and inflammation metabolic, genetic a proliments, are used to identify homologous sequences in other species; to detect the potentially more specific and less toxic than known immunosuppressants sources of antisense therapeutics. Modulators of LAT are potentially more specific and less toxic than known immunosuppressants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 340; DB 20;
Pred. No. 9.4e-65;
Disclosure; Fig 12A; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.0%;
Best Local Similarity 62.2%;
Matches 535; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of human Cbl.
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                                                                                                                                                                                                                                    gatotgactggcttatgtgaaccaactccccaagaccatatcaaagtgacccaggaacaa 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A gene encoding a cellulose synthetic equipment – for the improvement in the amount of cellulose synthesised in a plant body
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11.6%; Pred. No. 0.14;
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Matches 119; Conserv
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OJI PAPER (
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oligonucleotide; multiple target; antisense treatment; adenosine Al receptor antisense oligonucleotide fragment

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 tcatcttcagccacatgcacgcagagctgcacgcactcttccccgggggcaaagtactgtg
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The specification describes antisense oligonucleotides (X52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
non-coding regions of RNAs corresponding to target genes, gene
continitation codoss, genomic flanking regions, intron-exon borders, the
continitation codoss, genomic flanking regions, intron-exon borders, the
continitation codoss, genomic flanking regions between coding and non-coding
regions and all segments of RNAs encoding proteins associated with one
correct diseases, conditions or mixtures. The antisense oligonucleotides
may be derived from sequences X55180-271, can be used for the antisense
configuration of diseases and conditions. Typical diseases and conditions
are those associated with impaired respiration and inflammation,
concluding lung diseases, pulmonary vasoconstriction, inflammation,
concluding lung diseases, pulmonary vasoconstriction, emphysema, chronic obstructive
concluding vasociated variations and cancers, pulmonary
concern, hepatocallular carcinome, kidney cancer, lung cancer, pancreatic
concern, hepatocallular carcinome, kidney cancer, ung cancer, pancreatic
concern, hepatocallular carcinome, withous cancer, melanome, hepatic
concernsion, as well as all types of centers will and cancers and concerns and conc
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                                                                                                                                                                                                               pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114955: BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgtccgtgagtcccccttcgctgcgggacctgctgccccgcacagcgcagctgcttcgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastasized to the lungs, including breast and prostate cancer.
                                                                                                         impaired respiration; inflammation; lung disease; pulmonary vasconstitiction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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31.4%; Pred. No. 0.42;
live 66; Mismatches 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 37; 120pp; English.
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97US-0059160.
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Best Local Similarity 31.4
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                               prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild type and mutated sequences of Mycobacterium embCAB operon useful to e.g. identify ethambutol-resistant mycobacterial strains and produce antisense sequences to treat mycobacterial infections
                                                                                                                                                                                                                 Db 104358 gggcgcgccgccggccgggsnnndnnccgcbggccbgggcgcgccggccggccggsnnndn
                                                                                                                                                                                                                                                                                                                                                                                                           son properties of the second o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 accaccattgacctcacctgcagcgggcacgtgtccatcttcgagttcgacgtcttcacc
                                                                         182 aggtggcccattctcggcggcggcggcggcggaggcgccccggggggtcccggcggctctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium smegmatis embCAB operon.
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98WO-US05128
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P-PSDB; W73055-57.
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chambutol (EMB). It includes the embA, embC and embb genes that encode proteins, (see W7302-54) which are the target of action of M. smegmatis for EMB. To identify genes conferring EMB resistance, a genomic library from a high level EMB-resistant mutant of M. smegmatis as introduced into wild-type M. smegmatis mo2155. Four overlapping cospids were identified which conferred a resistant phenotype. The minimum size fragment capable of conferring EMB resistance was 9 kb (pIMM99). pIMM99 plus 7 kb upstream M. smegmatis sequence was dequences revelating 3 homologous open reading frames (embC, embB, embB) and 4 additional potential coding regions. Wild-type and mutated embCAB nucleic acid sequences are useful as probes used in the diagnosis of furqu-resistant mycobacteria infections; anti-DNA or anti-RNA sequences can be invention additionally provides for the use of embCAM operon conficience acid sequences as vaccines, or to improve existing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggccatcggctatgtgagctcagatggcagcatcctgcagaccatccctgccaacaaacc 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                         This is the DNA sequence of the Mycobacterium smegmatis embCAB
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0.31;
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Disclosure; Fig. 6A-I; 62pp; English.
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X53491/c
ID X53491 standard; DNA; 114955
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Matches 170; Conservative
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Db 104815 ccyegeccyegegnnhnnnsecccyegeccyegegnnhnnnsceccyegeccyegegnnhnn 104756
                                                                                                                                                                                                                                                                                                                         Db 104755 NSGCGCCCVGGCCVGCGGNNHNNNSCGCGCCCVGGCCVGCGGNNHNNNSGCGCGCCCVGG 104696
104875 HNNNSVGGCCVGCGGNNHNNNSCVGGCCVGCGGNNHNNNSCCVGGCCVGCGGGNNHNNNSC 104816
                                                                                 240 tggggactttctactcatctacctggccaatctggaggccaagagcagggaggtggccgc 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 004; ketolide; SAM synthase; S-adenosylmethionine synthase; hydroxylase; picromycin; antibiotic production; narbomycin; ds.
                                                                                                                                                                                                                                                Contig 004 from cosmid pKOS023-27 from Streptomyces venezuelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 104695 CCVGCGGNNBNNNSGCGCGCCVGGCCVNGCGGNNBNNNSC 104655
                                                                                                                                                                                                                                                                                                                                                                                                           360 actcaggcgacagctggccaagctggccatcttcagcc 400
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Z56005/
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directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and coding regions, intron-exon borders, the initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides (specifically X55180-271) can be used for the antisense coligonucleotides (specifically X55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leakenias, lymphomas, carcinomas e.g. colon cancer, breast cancer, melanoma, hepatic metastasses, as well as all types of cancers, melanoma, hepatic metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE 105055 GCGGCGCGCCCCVGGCCNHNNNNSCGGCCGGCGCGCGCGCGCGCCCVGGCCVNHNNNNSCG 104996
pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiration; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
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Best Local Similarity 31.9%
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                prostate cancer; ss.
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17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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/*tag= b
/product= ORF16_product
/note= "M. tuberculosis cbhK homologous partial protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is contig 304 from the recombinant cosmid pxoS023-27 DNA sequence (see 256001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (FKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. Polyketides are compounds synthesised from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                                                                                     Location/Qualifiers
complement (694..1692)
/*taq=
/*toduct= SAM_synthase
/note= "Partial S-adenosylmethionine synthase"
complement (3..692)
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98US-0141908.
98US-0100880.
99US-0119139.
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                                                                                                                                              Streptomyces venezuelae.
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P-PSDB; Y67216, Y67217.
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28-AUG-1998;
22-SEP-1998;
08-FEB-1999;
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62 ccctgggccgggcagtcaggatgctgcagcgcctagaagaagcaatgcgtcgaccccggc 121

Db 104935 CVGCNNHNNNSCGGCCCGGCCGGCGCGCCCCVGGCCVGCGNNHNNNSGGCCVGCGGNN 104876

180

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122 tgtccgtgagtcccccttcgctgcgggacctgctgcccgcacagcgcag--ctgcttcg 179

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Xue Y,

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Sherman DH,

WPI; 2000-160679/14. P-PSDB; Y77185.

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and two thioester domains. Four proteins make up the narbonolide PKS (PICAI, PICAII and PICAIV). PICAI includes the loading module and extender modules 1 and 2, PICAII includes extender module 3 and 4, PICAIII includes extender module 5 and PICAIV includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain. The second type II thioesterase domain is found on the PICA protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid pKOSO13-27. Narbonolide is desosaminylated in S. venezuelae to yield narbonovicin, the desosaminyl transferase enzyme is required for this conversion, and the desosaminyl transferase enzyme is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid pKOSO13-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human contractions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 809 getgtaetegeetgggggeagtgggeeateggetatgtgageteagatggeageateetge 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869 agaccatecetgecaacaaacceetgteceagtgeteetggagggacagaaggacgget 928
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    S. venezuelae desosamine biosynthetic gene desV, SEQ ID NO:15.

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                                                                                                                                                                                                                                                                                                                                                                    Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;
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1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 42.2;
48.9%; Pred. No. 1.
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1..1140
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/product= "DesV"
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287290/c
ID 287290 standard; DNA; 1140 BP.
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                                                                                                                                                                                                                                                                                                                           or veterinary medicine.
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Matches 113; Conserv
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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixromycin, neonethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells compourising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pixromycin, neonethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polykdroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful so biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., hardrais and antibiotics are active against a variety of organisms, e.g., hardrais and antibiotics are active against a variety of organisms, e.g., hardrais and all and a variety of organisms, e.g., hardrais and all and a variety of organisms, e.g., hardrais and antibiotics and adainst a variety of organisms, e.g., hardrais and antibiotics and adainst a variety of organisms, e.g., hardrais and a companisms.
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                                                                                                                                                                                    Desosamine and macrolide biosynthetic gene clusters, useful for, e .g. synthesis of methymycin and pikromycin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1125 CCGCTCGGCCCATTCGCGCACGGCGTCGATCACCCGCAGCGCCTGCGGGCGCTCCAGGTG 1066
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256004/c ID 256004 standard; DNA; 3291 BP.

256004;

(first entry) ✓ 23-MAR-2000

Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 003; ketolide; dNDP glucose synthase; dehydratase; picromycin; narbomycin; antibiotic production; ds. Contig 003 from cosmid pKOS023-27 from Streptomyces venezuelae,

Streptomyces venezuelae.

Location/Qualifiers

/*tage= a /*tage= a /product= dNDP_glucose_synthase /note= "glucose-1-phosphate thymidyl transferase" /*tag=

/product= PICCI /transl_except= (Pos:2874..2876, aa:Xaa) /note= "Xaa = Unknown" /product= dNDP_glucose4_6_dehydratase 2124..3263

WO9961599-A2

02-DEC-1999

99WO-US11814 27-MAY-1999; 98US-0087080. 98US-0141908. 98US-0100880. 99US-0119139. 28-AUG-1998; 22-SEP-1998; 28-MAY-1998 08-FEB-1999;

(KOSA-) KOSAN BIOSCIENCES INC.

ï Tang ď, McDaniel Betlach M, Betlach MC, Ashley G,

WPI; 2000-072618/06. P-PSDB; X67206, X67214, X67215.

New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -

Disclosure; Page 37-38; 98pp; English.

This is contig 003 from the recombinant cosmid pk05023-27 DNA sequence (see 256001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to the narbonolide polyketide synthase (PKS). The invention relates to combinant DNA containing a coding sequence for anarbonolide PKS.

CC recombinant DNA containing a coding sequence for anarbonolide PKS.

CC responsible for the production of many antibiotics including picromycin consists of a loading module, six extender modules, and two thioseter domains. Four proteins make up the narbonolide PKS and two thioseter domains. Four proteins make up the narbonolide PKS and extender modules a land 2, PICAII includes the loading module of and atype II thioseterase domain. The second type II thioseterase domain. The second type II thioseterase domain. The second type II thioseterase domain consideration on the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the accombinant commit pkOSO23-27. Narbonolide is desosaminalized in S. venezuelae to commid pkOSO23-27. The desosamine biosynthetic genes are also found in commid pkOSO23-27. The recombinant plosynthetic genes are also found in commid pkOSO23-27. The recombinant how then be converted (e.g. by cher enzymes recombinantly expressed in the same hosts) to polyketide artibiolics or their intermediates. The antibiotics are useful in human articles and a their intermediates. The antibiotics are useful in human and a second and or veterinary medicine

Sequence 3291 BP; 521 A; 1289 C; 1044 G; 436 T; 1 other;

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CGGTCGGCCCATTCGCGCACGCGTCGATCACCCGCAGCGCCTGCGGGCGCTCCAGGTG 3188 ctgcagcgcctagaagagcaatgcgtcgaccccggctgtccgtgagtccccttcgctg 145 cgggacctgctgccccgcacagcgcagctgcttcgagaggtggcccattctcggcggcg 3187 cadaccearcaccangadaccraccacacaaacarcaccacacaaacaaacca 3127 TICCGGCGGTGCCTCGCCCGCGTAGGCGGGCGAGAGGTGCACGGGTACCGGGTAGTGCGT gccggcggaggcgcggggggtcccggcggctctgggggactttctactcatctacctg gccaatctggaggccaagagcaggcaggtggccgcgctgctgctccccgggggccgaagg ö Length 3291; Score 41.6; DB 21; Pred. No. 2.7; 0; Mismatches 159; 2.78; Similarity 46.3 7; Conservative Matches 137; Query Match Best Local 3247 3067 82 265 õ a g ò

287284 standard; DNA; 12441 BP

S. venezuelae desosamine biosynthetic gene cluster pikB, SEQ ID NO:3.

99WO-US14398 25-JUN-1999; 98US-0105537

(MINU) UNIV MINNESOTA.

synthesis of methymycin and pikromycin

The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster in Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin,

GAGGGTGTCGATGCCGCGGGGGTCGAGGTGGCTGCGCAGCTCGTCGCGGCGCCTCGGTGCG 325 agigocaacgacgagetetteegggegggeggeteeagaeteaggegaeagetggeeaa 380

à

RESULT Z87284

(first entry) 05-JUN-2000

Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; orop protection agent; ds.

Streptomyces venezuelae ATCC15439

WO200000620-A2.

06-JAN-2000.

26-JUN-1998;

Xue Y, Liú H, Sherman DH,

ä Zhao

> WPI; 2000-160679/14 P-PSDB; Y77179.

ρ. . Desosamine and macrolide biosynthetic gene clusters, useful for,

Claim 2; Page 281-287; 438pp; English.

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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea.or streptomyces antibloticus. The invention also relates to a macrolide biosynthetic gene cluster. Or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and conform macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pixromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polykydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as blopolymers, e.g., in packaging or biomedical applications, to
                                                                                                                                                                                                                                                                                                                                                       ./product= "PixB gene cluster protein #6 (Y77208)"
/note= "No termination codon given in the specification"
/transl_except= (pos:8270..8272, aa:Yal)
/transl_except= (pos:8273..8275, aa:Thr)
-/transl_except= (pos:8276..8278, aa:Gly)
complement (10126..11139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product= "PikB gene cluster protein #10 (Y77211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "PikB gene cluster protein #11 (Y7212)"
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complement (7942..8205)
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/product= "PikB gene cluster protein #7 (X80999)"
complement (11271...12149)
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                         /product= "PikB gene cluster protein #2 (Y80998)'
                                                                                            gene cluster protein #3 (Y7205)"
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P-PSDB; Y77204, Y77205, Y77206, Y77207, Y77207, Y77208, Y77209.
Y77210, Y77211, Y77212, Y80998, Y80999.
                                                                                                                                                                  gene cluster protein #4 (pos:6837..6841, aa:Gln)
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complement (13706..15043)
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/transl_except=
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6834..7402
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pikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the descamine and/or marcolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antiblodics and polyhydroxyalkanoate (PHA) as biopolymers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide based and antiblotics which are active against a variety of organisms, e.g., p. 100.
                                                                                                                                                                                                                                                                                                                                   bacteria, including multi-drug resistant pneumococi and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster from Streptomyces venezuelae ATCC 15439.
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/note- "No initiation codon given in the specification"
806..2014
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Pred. No. 3.5;
0; Mismatches 159;
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Best Local Similarity 46.3%;
Matches 137; Conservative (
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287319;

CDS

RESULT 10

287319 G

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engineer PHA monomer synthases or to prepare biologically active agents, such as chamotherapeutics, immunosuppresants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, as given in figure 32.
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Sequence 13613 BP; 1858 A; 4733 C; 5092 G; 1930 T; 0 other;

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                                Gaps
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Pred. No. 3.6;
0; Mismatches 159; Indels
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Query Match
Best Local Similarity 46.3%;
Matches 137; Conservative
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FIP; FADD interacting protein; FADD; Fas-associated protein with a novel death domain; cell death; apoptosis; Alzheimer's disease; Acquired Immune Deficiency Syndrome; ALDS; muscular dystrophy, amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasm; protozoa; neoplasia; dysplasia; hyperplasia; ds.
                                                                                                                                                   Location/Qualifiers
                                                Human FADD protein coding sequence.
                             (first entry)
                                                                                                                                Homo sapiens
                              27-APR-1999
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/*tag= a /label= Human_FADD_protein 969.. WO9900499-A1 Key

07-JAN-1999,

26-JUN-1998;

98WO-US13320

98US-0087886. 03-JUN-1998; 26-JUN-1997;

CORP (CHIR) CHIRON

Williams LT; Chen II,

1999-095745/08. WPI; 1999-0957, P-PSDB; W96154

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New FADD (Fas-associated protein with a novel death domain)-Interacting Protein - useful for inducing or preventing apoptosis in a cell, to aid in controlling apoptosis-related diseases

Disclosure; Page 45-46; 58pp; English.

An epitope of human FADD (Fas-associated protein with a novel death domain)-Interacting protein (FIP protein) comprising amino acids 348-727 of the protein described in W96153, can be used to induce or prevent apoptosis in a cell. Specifically, decreasing the levels of FIP348-727 prevents apoptosis. This is useful in cells which are dying prematurely, eg: Alzheimer's disease, Acquired immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic alteral sclerosis (and other muscle wasting diseases) autoimmune diseases, and diseases where cells are infected with a pathogen (virus, bacteria, fungus, myopulasm or protozoa). Increasing the levels of FIP 348-727 induces apoptosis which is useful in cells suffering from meoplasias, dysplasias, hyperplasias, or their symptoms. Purified and isolated FIP subgenomic polymucleotides are useful as primers to obtain more copies of the nucleotides, and as probes that identify wild-type or mutant coding sequences. They are also useful for expressing FIP man, proteins or fusion proteins, and in the generation of FIP manisense cligonucleotides and in the generation of FIP manisense cligonucleotides and in the generation of FIP manisense cligonucleotides and an electron of FIP mans and in constructs and in gene delivery vehicles (optionally in combination with a condensing agent) that deliver FIP mRNA or oligonucleotides, FIP proteins antibodies into eukaryotic cells. This is the human FADD protein gene. Human FIP protein lin W96154.

Sequence 1582 BP; 344 A; 433 C; 483 G; 322 T; 0 other;

Gaps ö 20; Length 1582; Indels Score 41.4; DB 20; Pred. No. 2.5; 0; Mismatches 116; 2.7%; Query Match
Best Local Similarity 48.9
Matches 111; Conservative

0

93 cctagaagaagaatgcgtcgacccccggctgtccgtgagtcccccttcgctgcgggacct 152 gtggggggggacagtgggaagaggcccgcgccctgggccgggcagtcaggatgctgcagcg 156 gogogtgggcaagogcaagotggagoggggggggggggctagacotottctccatgct 216 getggageagaacgaectggageeegggeacacegageteetgegegagetgetegeete 33 Dp g δ ŏ

153 getgeecegeacagegeagetgettegagaggtggeeceatteteggegggegggegg ŏ 셤

336 ggccgccctggggaagaagacctgtgtgcagcatttaacgtcatat 382 213 aggoggococgggggtcocggoggctctgggggacttctactcatct δŽ 엄

RESULT 12 T39397

T39397 standard; cDNA; 1642 T39397; XXEXEXEX

novel death domain) FADD (Fas-associating protein with

(first entry)

22-FEB-1997

Human; FADD; Fas-associating protein with novel death domain;

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apoptosis; Fas regeptor; death domain; gene therapy; antibody; immunoassay; drug screening; diagnostic; AIDS; antiinflammatory; antitumour; cerebroprotective; neuroprotective; ss.

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The sequence encodes FADD (Fas-associating protein with novel death domain), which binds the cytoplasmic region of a Fas receptor, and modulates apoptosis induced by activation of the receptor by ligand binding. The CDNA has been isolated using a yeast two-hybrid system which screens for proteins interacting with the Fas cytoplasmic sytoplasmic domain. A GALA DNA-Dhading domain has been fused to the human Fas antigen cytoplasmic tail to form a bait plasmid, which is used with a prey plasmid, containing a human B-lymphocyte cDNA library fused to cover lapping clones 8 and 15 have been isolated, and the full-length cDNA has been isolated from a human umbilical vein endothelial cell in-frame stop codon 130 by upstream of the initiator Met. The cONA domain of Fas. The DNA may be used in gene therapy, and the protein or a corresponding antibody may be used to screen for apoptosis, for use in therapy of e.g. AIDS, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FADD protein that binds to cytoplasmic region of Fas receptor identifying inhibitors of Fas-associated apoptosis useful for treating e.g. AIDS, leukaemia, stroke, etc
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note= "Region encoding death domain"
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/oote= "Encodes N-terminal half, indu
foote= but not binding Fas receptor"
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note= "Clone 15 start point"
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/note= _In-frame stop codon"
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"Clone 8 start point"
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                                                                         location/Qualifiers
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95US-0416379.
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03-APR-1995;
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                                                                                                                                                                                  275
                                                                                                                                                                                                                   cctagaagaagcaatgcgtcgaccccggctgtccgtgagtccccttcgctgcgggacct 152
                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                   336 cetgeggegewacgacetgetgeggegegtegacgacttegaggegggggggggeggegg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human homologue; Drosophila fused gene; intracellular signal;
human hedgehog-patched protein; HH-PTC; RNA transcription;
RNA translation; cancer diagnostic; prophylaxis; karotyping analysis;
cancer; embryonic repair; tissue repair; wound healing;
neurodegenerative disease; testicular function; ss.
                                                                                                                    Gaps
                                                                                                                                                  33 gtgggggggaaagtgggaagaggcccgcgccctgggccgggcagtcaggatgctgcagcg 92
                                                                                                                                                                                    216 gegegtggggaageggaagetggagegegtgeagageggeetagaeetetteteeatget
                                                                                                                                                                                                                                                                                     cDNA encoding a protein involved in eliciting a signal in HH-PTC
                                                                                                                ;
                                                                                 Length 1642;
leukaemia, myocardial infarction, degenerative disease, etc
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                         213 aggoggecegggggteeeggeggetetgggggaetttetaeteatet 259
                                 Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 other;
                                                                                 Score 41.4; DB 17;
Pred. No. 2.6;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human homologue of the Drosophila fused gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 74-77; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X81941 standard; cDNA; 2644 BP
                                                                                 2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-SE02384.
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                                                                                                                Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-418918/35.
P-PSDB; Y23755.
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9932609-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toftgard R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
X81941
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                                                                                                                                                                                                                                                                                     inducing apoptosis
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detection and quantification of normal or abnormal fused gene sequences. The labeled probes can also be useful in karctyping analysis as markers of the fused gene. The polynucleotides may also be used in gene therapy methods. The polypeptide is useful as a lead compound in the design of analogues and mimics, as well as for screening for agonists and antagonists. The products may also be used for the study of different conditions, such as cancer and development of cancer therapies, the regulation of gene transcription, embryonic repair and tissue repair/wound healing, neurodegenerative diseases, and testicular
                                                                                                                                                                                                                                                                    function.
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WPI; 1999-527456/44. P-PSDB; Y57456.

ロロノ ボウザールコーのゴ

0007 *0:TT:00 8

Err Dec

Sequence 2644 BP; 542 A; 780 C; 755 G; 567 T; 0 other;

2.7%;

Query Match

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                                                                                                                                                                                                                                                     gigagicoccettogotgoggacotgotgoccogoacagogcagotgottogagaggig 186
                                          Gaps
                                                                                99
                                                                                    geteceatggetetggeggtggeeegtgggggegaeagtgggaaggeeegegeeetg
                                                                                                                                                                                                                                                                                              1395 ctgcttcacactgaggttcagaacctcatggcccgagctgaatacttgaaggagcagatg
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Score 41.4; DB 20; Length 2644;
Pred. No. 2.8;
); Mismatches 121; Indels 0;
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                    Best Local Similarity 48.5
Matches 114; Conservative
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Human; fishboy; G-protein coupled receptor; therapy; diagnosis; signal transduction; HIV; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; unimary retention; stroke; osteoporosis; angina pectoris; myocardial infarction; myaraine; ulcer; allergy; benign prostatic hypertrophy; vomiting; dyskinesia; psychotic disorder; neurological disorder; Huntington's disease; Tourette's syndrome; ss.
                                                                                              Human fishboy G-protein coupled receptor encoding cDNA.
                                                                                                                                                                                                                                         Location/Qualifiers
1..1170
                       ВР
                       Z39042 standard; cDNA; 1170
                                                                        (first entry)
                                                                                                                                                                                                                        Homo sapiens
                                               239042;
RESULT 1
Z39042/c
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ВР
                                                                                          (first entry)
                                             138913/c
ID 138913 standard; DNA; 880
                                                                                         15-MAY-1997
                                                                       T38913;
                                     RESULT
                                                               MAX DX DX SX MX
/*tag= a
/product= "Fishboy"
/note= "a G-protein coupled receptor"
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                                                                                                                      SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                         98US-0075626.
98US-0133132.
                                                                         99WO-US03246.
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Elshourbagy N,

W09942484-A1

16-FEB-1999; 20-FEB-1998; 13-AUG-1998;

26-AUG-1999

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The present sequence encodes a human G-protein coupled receptor, designated Fishboy Fishboy products can be used to treat subjects in need of modulated Fishboy expression or activity. Diseases or disorders to be treated include bacterial, protozoal, fungal and viral, particularly HIV-1 or HIV-2 infections, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, apportension, hypertension, uninary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcars, allergies, benden prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders and dyskinesias such as Huntington's disease or Tourette's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B2-bradykinin receptor gene exon 3 polymorphic region, allele BE3-R48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 tggcggtggccccgtgggggggacagtgggaagaggcccgcgccctgggccgggcagtca 79
                                                                 e.g. benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 C6CGCCCCGTGCCGCCCGGAGCCCCAGCGGGCGCCCCGGCAGCCGTGCCAGCGTCACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 TAGCAGCCGAGCATCAGCCCGAAAGGAAGCACGAAAGCGGTCAGAGTCTCCAGGCTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 TGGGCGGCGGGGCGTGGCGCGGGGGGGCGCACGCGGTGGCATACGCGGTCCCTCCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgaaggagtgccaacgacgagctcttccgggcgggctccagactcaggcgacagctggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 AGGCAGCGCT3CAGGCTGAGCAGGCCGGTGAGCAGCACGCTGGCGTGACATGCTGAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             815 TGGTAGGGGGCCCAGAGCAAGCCGAAGCAAGCACGATGGCGCTCACCAGCCGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.2; DB 20; Length 1170; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tandem repeat polymorphism; B2 bradykinin receptor; diagnosis; myocardial infarction; coronary heart disease; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aagtactgtggacacatgtaccagctcaccaaggccccgcccacacattctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                     A new G-protein coupled receptor, Fishboy used to treat, prostatic hypertrophy -
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1170 BP; 137 A; 409 C; 415 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                       Claim 2; Page 34-35; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%;
Best Local Similarity 44.3%;
Matches 210; Conservative
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Query Match 2.6%; Score 40.4; DB 17; Length 880; Best Local Similarity 53.1%; Pred. No. 3.7; Matches 86; Conservative 0; Mismatches 76; Indels 0;
                               Location/Qualifiers
117..841
                                                                                                     /rpt_type= TANDEM
                                                                /*tag= b
/label= BE3-48R
                                                                                                                                                                                                               Claim 4; Fig 3; 13pp; German
                                                                                                                                     95DE-1018931
                                                                                                                                                95DE-1018931
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/*tag= c
                                                                                                                                                                     Kammerer S;
                                                                                                                                                                               WPI; 1996-426182/43.
                                                                                                                                                          (ROSC/) ROSCHER A.
                                     repeat_region
                                                                                                               DE19518931-C1
                                                                                                                                               23-MAY-1995;
                                                                                                                                    23-MAY-1995;
                      Homo sapiens
                                                                                           repeat_unit
                                                                                                                          19-SEP-1996
                                                                                                                                                                     Braun A,
                                                           allele
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The present sequence represents allele BE3-R48 of the tandem-repeat polymorphic region of exon 3 of the B2-bradykinin receptor gene.
Two alleles have been identified; allele BE3-48R contains 48 tandem copies of repeat units with the consensus sequence rGGA(A)GGCTAGAACC, while allele BE3-35R contains 35 copies.
TGGA(A)GGCTAGAACC, while allele BE3-35R contains 35 copies.
The polymorphic sequences are useful for diagnosis (i.e. relating frequency of a potymorphism to disease occurrence) and/or treatment of myocardial infarction; coronary heart disease; sterility; hypertension; genetically related vascular disease; sterility; and acute or chronic inflammation. They can also be used to test potential drugs against such diseases and pharmaceuticals that contain and bradykinin (ant)agonists.
hypertension; genetically related vascular disease; sterility; infertility; atopia; asthma; allergy; altered bronchial reactivity; acute; chronic; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "alternative allele BE3-35R contains 35
tandem repeats with the consensus sequence
TGGA(A)GGGCIAGAACC"
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                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "contains 48 tandem repeats with the
consensus sequence TGGA(A)GGGCTAGAACC"
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0; Gaps

1023 getgcagetetactgggecatggactecacatttgagetetgcaagatetgtgetgagag 1082

401 GITCIAGCICICCAGGITCIAGCCCICCAGGITCIAGCICICCGAGITCIAGCCCICCAG 342

341 GIICTAGCICICCGAGIICTAGCCCICCAGGIICIAGCCCICCAGGIICTAGCICICCAG 282

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281 ATTCCAGCCTCCAGGTTCTAGTCCTCCAGCTTCTAGCTCAG 240

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AUTHORS
TITLE
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220097 HGAAABKEX T
C12082 C12082 Yuji
AL011383 F.rubripe
AL053013 Drosophil
AL01361 F.rubripe
AL066742 Drosophil
AL066742 Drosophil
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AW268166 Xr93a08.X
A1344947 Lb01c03.X
AL108460 Drosophil
AW301448 XS77a09.X
AW301461 XS77c05.X
                                                                                                                                                                              AA112513 ZMZ8C07.T
AW456122 59653 MAR
AA113289 ZMZ8C07.S
A1368245 qw16f09.X
F22931 SSC17A01 PO
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BE283475 0C1102508
AW935651 RC3-DT01
AI758472 ty08b03.x
AW756557 RC4-UM03
AI388785 GH19792
AI801220 to86c10.x
BE01124 VVO BT004
C69305 C69305 Yuji
AL110451 DKFZp434F
AV38228 AV98238
BE201648 fX96607.x
D68728 CELK055AYF
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A1345656 tb78f04.x
A1344839 tb99909.x
A1345593 tb78d02.x
AW302967 xr87c06.x
                                                                                                                                       A1660567 we68c03.x
BE407909 601299249
BE464228 hv84h11.x
BE198430 ug78e05.y
A1690580 tg02a11.x
AW463722 BP2300138
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AL053013 Drosophil
                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            Description
                                                                                                        SUMMARIES
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AI345656
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 751)
Nolicomer Testitute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg@nih.gov
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lnli.gov) for further information.
Insert Length: 864 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 458.

1. 751m.maces stop: 458.

1. 751m.maces stop: 458. 3; /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2346244"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo. 5 others A1660567 751 bp mRNA EST 18-DEC-1999 we68c03.xl Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346244 3' similar to TR:Q13193 Q13193 CBL-B TRUNCATED FORM gcagctctactgggccatggactccacatttgagctctgcaagatctgtgctgagagcaa 1073 1013 532 cctggagggacagaaggacgtctctacctctacccagatggaaagacccacaaacccaga 953 514 835 agctcagatggcagcatcctgcagaccatccctgccaacaacaccctgtccc-aggtgct 893 Gaps ggcagttacatcttccggcccagctgtactcgcctgggggcagtgggccatcggctatgtg cetgaettgageteggeeaggeageececageagegeatecacqtgteagaggageaget 572 cergacreagereggeagaa-eccageagerecerecaegrereageageager .; m Similarity 94.6%; Score 564.8; DB 12; Length 751; Similarity 94.6%; Pred. No. 1.5e-120; Conservative 0; Mismatches 32; Indels 3; AI660567.1 GI:4764137 AI660567 disease human. 614; Query Match Best Local 8 LOCUS 954 δŽ Dp ò

1014

us-09-434-708-3.rst

Length 695;

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamaala; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1 (base 1 to 695)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

NAH-MGC linstitutes of Health, Mammalian Gene Collection (MGC)

Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-11550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: ATCC
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Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM315 row: b column: 14 High quality sequence stop: 686.

Location/Qualifiers
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BE407909. GI:9344359
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NCI-OGAP, http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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39.0%; Score 554; DB 35; ilarity 94.0%; Pred. No. 4.8e-118; Conservative 0; Mismatches 30;
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                                                                                                                                              Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Duck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@lange.llnl.gov
Seq primer: -400P from Gibco
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand CDNA was prepared from mammary palnd tissue from a lactating femele, and was then primed with a Not I - Oilgo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 533) NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
BE198430 533 bp mRNA EST 26-JUN-2000 Y1 Soarses_mannary_gland_NMLMG Mus musculus cDNA clone IMAGE:1546512 5' similar to gb:X57110 PROTO-ONCOGENE C-CBL (HUMAN ); mRNA:sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:953860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="INAGE:1548512"
/clone_lib="Soarse_mammary_gland_NMIMG"
/sex="Emale (lactating)"
/tissue_type="nammary gland"
/lab_host="DH10B"
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High quality sequence stop: 466.
Location/Qualifiers
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us-09-434-708-3.rst

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Tumor Gene Index
Unpublished (1997)
Contact: Robert_Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmart-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayade Dy: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lln.gov/Abrpy/Amage.inmal
Seq primer: -40UP from Gibco
High quality sequence stop: 381.
Location/Qualifiers
1. 530
Location/Qualifiers
1. 530
Location/Qualifiers
2. pooled tumors"

//Lissue_type="Poorly-differentiated endometrial
adenocarcinome, 2 pooled tumors"
//Lissue_type="Poorly-differentiated endometrial
adenocarcinome, 2 pooled tumors"
//lab_host="DHIOB" NCI_CGAP_UT3"
//lab_host="DHIO
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI690580 530 bp mRNA EST 27-MAY-1999 tq02a11.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207612 3' similar to TR:Q13193 Q13193 CBL-B TRUNCATED FORM 2, ;, mRNA
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                                                                                                                                                                                     1054 aagatctgtgctgagagcaacaaggatgtgaagattgagccgtgcgggcacctgctctgc 1113
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994 cacqtqtcaqaqqqaqcaqctqcaqctqqqcatqqqqcatqqactccacatttqaqcttqtq
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Tell 11. 21. 333 5998

Fax: 217 244 5617

Email: h_lewinGuiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research.Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Wonack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 440)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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BP230013B10F1 Soares normalized bovine placenta Bos taurus CDNA
clone BP230013B10F1 5', mRNA sequence.
AW463722
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                                                                                                                                                                                                                                                                                          gigaccaggaaggcagggagitggagciggggcaggigccctitcggctcctccatigc 1309
                                                                                                                                                                                                                                                                                                                                                                                               Bovine ESTS
Uppublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                335
                                                                                                                                                                                                                                                                                                                         /note="Organ: placenta; Vector: pT7T3Pac; Site_1: Site_2: Not1; The cDNA library was contributed by
                                                                                                                                                                                     1190 aggeegtgagtatetaceagttecaeggteaggetaetgetgaggaeteagggaacaggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="bos taurus"
/db_xref="taxon:9913"
/clone="mb730013810F1"
/clone_lib="Soares normalized bovine placenta"
/lab_host="DH10B"
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BACKWARD: ATTAACGCTCACTAAAG
INSERT LENGTH: 440 Std Error: 0.00
Plate: B£230013B10 row: F column: 1
Seq primer: AGGGAPTACAATTTCACACAGGA
High quality sequence stop: 440.
Location/Qualifiers
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1 (bassa 1 to 435)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DiBuque,T., Favello,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevsskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA112513 435 bp mRNA EST 23-DEC-1997
2m28c07.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone.
IMAGE:526956 5' similar to gb:X57110 PROTO-ONCOGENE C-CBL (HUMAN);
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Soares laboratory and it was constructed and normalizas described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "142 c 120 g 78 t
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                                                                                                                                                                                                                                                                      CTGGGGAAGTGGGCCATCGGATACGTGAGCTCAGACGGCAGCATCTTGCAGACCATCCCT
                                                                                                                                                                                                                                                                                                    gocaacaaacccctgtcccaggtgctcctggagggacagaaggacggcttctacctctac
                                                                                                                                                                                                                                                                                                                                                                                                                               cgcatccacgtgtcagaggagcagctgcagctctactgggccatggactccacatttgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                           Length 440;
                                                                                                                                             Indels
                                                                                                           Score 370.8; DB 22;
Pred. No. 1e-75;
0; Mismatches 42; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AA112513
AA112513.1 GI:1665062
                                                                                                           26.1%;
90.4%;
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hes 396;
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Matches
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                                                COUNT
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Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
WARNING: There is evidence that suggests that the 384-well parent blate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality; sequence stop: 336.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823 atoggetatgtgageteagatggeageateetgeagaceateetgeeaacaaacaeeetg
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taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 356.2; DB 1;
Pred. No. 2.5e-72;
); Mismatches 20;
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AW426122:
AW426122:1 GI:69540FO
EST
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ilarity 94.1%;
Conservative 0
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AUTHORS

JOURNAL COMMENT

TITLE

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota, Metazoa, Chordata, Craniata, Hominiaae, Homo.

1 (bases 1 to 462)
1 (bases 1 to 462)
1 Hiller,L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Ghissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,S., Morie,M., Paragoe,C., Riffith,L., Rohlfing,T.,
Schellenberg,K., Scares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314.286 1800
Email: est@watson.wustl.edu
WARNING: finere is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should is
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40Ml3 fwd. from Amersham High quality, sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1054 aagatetgigstgagageacaaggatgigaagattgageegigeggeeectgetege 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggactcagggaacagcagtgaccaggaaggcagggagttggagctgggggcaggtgccct 1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 AGCTGCTGCCTGGNTGCCTGGCAGCACTCGGACAGCCCAGACCTGCCCCTTCTGCCGCTG
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                           GI:1664994
                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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AA113289.1
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Matches 349
                         VERSION
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JOURNAL
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AUTHORS
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Smith.T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keele-J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Contact: Smith TPL
CODDA, ARS, US Meat Animal Research Center
DO BOX 166, Clay Center, NE 68933-0166, USA
Tel: Smith TPL
CODA, ARS, Govern and Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: Smith TPL
CODA, ARS, Govern and Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: Smith TPL Coda gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR PRIMERS
FORWARD: GTTTCCCAGTCACGACG
PRIMERS
FORWARD: GTTTCCCAGTCACGACG
PLATE GOLUMN: 8
Seq primer: ATTAGGTGACACATARG.
Seq primer: ATTAGGTGACACATARG.
Location/Qualifiers
1.rce
And ALSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtgtcagaggagcagctgcagctctactgggccatggactccacatttgagctctgcaag 1056
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 336.2; DB 22; Length 428; Pred. No. 1e-67; 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1057 atctgtgctgagagcaacaaggatgtgaagattgagccgtgcggg 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="ware 4Bov"
/tissue_type="pooled"
/lab_host="DH10B"
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ilarity 89.4%;
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133 c
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Best Loca Matches

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BASE COUNT ORIGIN

FEATURES

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RESULT 9
AA113289/c
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DEFINITION

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241 AACAAGGACGIGAAGATIGAGCCAIGCGGGGCACIGCTGTGCAGCCCGCTGCCTGGGCTA 300
 178 GGGAACAGCAGTGACCAGGAAGGCAGGGAGTTGGAGCTGGGGCAGGTGCCCCTTTCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .491
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="c17a01"
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Sus scrofa
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Matches 282;
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Conteact: Rebert Strausberg, Ph.D.

Tel: (301, 496-1550

Tal: (301, 496-1550

Tal: (301, 496-1550

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbpf/Amage/image.html

Insert Length: 648 Std Error: 0.00

High quality sequence stop: 359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. :398
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="Laxon:9506"
/clone=lib="NCI_CGAP_Ut3"
/clone=lib="NCI_CGAP_Ut3"
/tissue_type="poorly-differentiated endometrial
adenocarcinome, 2 pooled tumors
/lab_host="DBIOB"
/lab_host="DBIOB"
/lab_host="DBIOB"
/site_1: Noti: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP inttp://www.ncbi.nlm.nih.gov/ncicgap.
Thinor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                       AI368245 398 bp mRNA EST 15-FEB-1999 qw16f09.xl NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991273 3' similar to TR:013193 Q13193 CDL-B TRUNCATED FORM 2', contains PTR5.t3 MER22 repetitive element ;, mRNA sequence.
AI368245 GI:4137990
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                                                     162 GCCGAAAGTGAGACTCCTAAAGGGGAACT-CCCNCNTCNTGCGCTGGGACCCCAGGACNC 104
222 TINGGCTCCTCCATIGCCCCCACGGCCAGATCTGCCCCCAGGAAGCCCAGAAATGCCCA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                     1353 gccgaaagtgagactcctaaaggggaactcccctccagctgcgctgggaccccaggaccc
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21.2%;
Best Local Similarity 99.7%;
Matches 302; Conservative
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                                                                                                           1413 tgccccggc 1421
                                                                                                                                                103 NCTNCCCGC 95
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SSC17A01 Porcine small intestine cDNA library Sus scrofa cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: A.K. Winteroe
Department of Animal Science and Animal Health, Division of Animal
Genetics, The Royal Veterinary and Agricultural University
Bulowsvej 13, 1870 Frederiksberg C, Denmark.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases 1 to 491)
Wintero, A.K., Fredholm, M. and Davies, W.
Fredholm, M. and Davies, W.
Fredholm, and Characterization of a porcine small intestine cDNA library; analysis of 839 clones
Mamm., Genome 7 (7), 509-517 (1996)
                                                                           1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1072 aacaaggatggaagattgagccgtgcgggcacctgctctgcag--ctgctgcctgctg 1129
                      cotocattgccccacggccagatctgcccccaggaagcccagaaatgcccagccgaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Porcine small intestine cDNA library"
/note="directionally cloned cDNA in XLI-blue MRF'"
1 142 c 145 g 79 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832 gtgagotcagatggcagcatcctgcagaccatccctgccaacaacccctgtcccaggtg
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60;
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Pred. No. 3.3e-44
0; Mismatches 6
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us-09-434-708-3.rst

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EST.

BUSATORS.

Mus musculus

BUKARYOTGS, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

BUKARYOTGS, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musculus

I (bases 1 to 545)

I (bases 1 to 545)

NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.

NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.

NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.

NIH-MGC i (1999)

AL Unpublished (1999)

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tel: (301) 496-1550

CONTECT: Robert Strausbergenih.gov

Tel: (301) 496-1550

CONTECT: Robert Strausbergenih.gov

Tel: (301) 406-1550

CONTECT: Consortium (LINL)

DNA Stepenching by: Incyte Genomics, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Stepenching by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Algh quality sequence stop: 542.

S I.C.

Corganism="Mack: Robert I (feral)"

Algh xref="Mack: Robert I (fera
                                                                                                                                                                                                                                                                                                 BE283475 545 bp mRNA EST 13-JUL-2000
051102508F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495025 5',
mRNA sequence.
BE283475
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Site_2: Not1; Cloned unidirectionally, Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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ilarity 70.2%; Pred. No. 2.2e-33;
Conservative 0; Mismatches 142; I
                                                                                                           488 AGCCGIGCGGCACCIGCICIAGAGCIGIICGCIAGGIGCCI
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Eukaryota, Matazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Matazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 529)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneal,C.V., O'Hare
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                               AW857217 529 bp mRNA EST 19-MAY-2000 RC2-CI0304-120200-012-e10 CI0304 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      971 aggoagaaccccagcagcgcatccacgtgtcagaggagcagctgcagctctactgggcca 1030
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Pred. No. 1.2e-34;
0; Mismatches 18; Indels 0;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
Brazil
          1130 cetggcagcactcggacagccagacctgccccttctgccgctgc 1173
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/clone_lib="Droll"
/dev_stage="Adult"
/note="Organ: denis_drash; Vector: pucl8; Site_l: SmaI;
Site_l: SmaI, A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
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I bases 1 to 420,
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                    AW935681 420 bp mRNA EST 30-MAY-2000 CAS-200017-180200-012-e10 DT0017 Homo sapiens cDNA, mRNA sequence. AW935681. GI:8111087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgum sequencing of the human transcriptome with ORF expressed sequence tags
Proc. U.S.A. 97 (7), 3491-3496 (2000)
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Fax: +55-11-2707001
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REFERENCE AUTHORS MEDLINE COMMENT

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Pred. No. 1.6e-32;
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ilarity 68.8%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases; 1 to 258)

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Au Coppolished (1997)

Tumor Gene Index

Oppublished (1997)

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Stef Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Insert Length: 1575

Seq Primer: -400P from Giber: 0.00

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Seq Primer: -400P from Giber: 0.00 AI758472... 258 bp mRNA EST 16-DEC-1999 ty08b03.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2278445 3' similar to contains PTR5.t3 MER22 PTR5 repetitive element ;, mRNA AI758472.1 GI:5152195

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BE198430 ug70e05.y
AL136284 qw/16f09.x
AAL13289 arm28007.s
AAL12513 arm28007.s
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F22931 SCC17A01 PO
AW857217 RC2-CT030
BEE8475 RC1-CT030
AW935681 RC3-DT001
AI34447 LD01C03.x
AW301388 xs75C04.x
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AI345556 LD7840.x
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'n /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2346244"
/clone=lib="Soares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease" A1660567 751 bp mRNA EST 18-DEC-1999
we68c03.::1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
1. i, mAGE:2346244 3' similar to TR:Q13193 Q13193 CBL-B TRUNCATED FORM
A1660567 cotgactgagutoggccaggcagaaccccagcagcgcatccacgtgtcagaggagcagct 1025 ggcagttacatcttccggcccagctgtactcgcctgggggcagtgggccatcggctatgtg 846 905 514 AGCTCAGATGGCAGCATCTTGCAGACATCCTTGGCCAACAACNCCTGTTCCCAAGGTGCT 632 cetggagggadagaaggacggettetacetetacceagatggaaagacecacaacaga 965 ageteagatggeageateetgeagaceateettgeeaacaaaceetgteee-aggtget 572 ccrgacreacreggecagecagaa-eccagecarecareargreagagagager 43.2%; Score 668.8; DB 12; Length 751; 95.4%; Pred. No. 3.5e-146; cive 0; Mismatches 32; Indels 3; /lab_host="DH10B (phage-resistant)" AI660567 1 GI:4764137 Conservative Similarity human. Best Local Sim Matches 718; Query Match source DEFINITION ORGANISM BASE COUNT REFERENCE AUTHORS TITLE 691 787 847 906 996 ACCESSION JOURNAL VERSION KEYWORDS FEATURES COMMENT g δŏ g Dp qq Qγ δŽ

F.rubripe Drosophil AL262733 Tetraodon AL011383 F.rubripe AL053013 Drosophil AL053013 Drosophil AL066051 Drosophil AL066742 Drosophil Drosophil Z20097 HSAAABKFX T C12082 C12082 Yuji

ALIGNMENTS

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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tels: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: The I.M.A.G.E.
CDNA Library Arrayed by: The I.M.A.G.E.
CONSORTIUM (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM315 row: b column: 14
High quality sequence stop: 686.
High quality sequence stop: 686.
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( Dases 1 to 695)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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//organism="Homo sapiens"
//orone="IMAGE:3629101"
//olone="INH-MGC2:3629101"
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//issue_type="choriocarcinoma"
//lab_host="DH10B (phage-resistant)"
//ore="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
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clone IMAGE:3629101
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                                      93 GCACCCAGAIGIGCTIGCTCAAGGGACCCCCAAGGGCTGGAAGGGGTTGTAAAACCGAAA
                                                                                             gcagcactoggaccagacctgccccttctgccgctgcgagatcaagggctgggaggc
                                                                                                              393 GCAGCACTCGGACAGCCAGACCTGCCCCTTCTGCCGCGTGCGAGATCAAGGGCTGGGAGGC
                                                                                                                                                     1206 cgtgagtatctaccagttccacggtcaggctactgctgaggactcagggaacagcagtga
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601299249F1 NIH_MGC_21 Homo sapiens CDNA
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BE407909.1 GI:9344359
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following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE464528 522 bp mRNA BST 27-JUL-2000 hv84h11.x1 NCI_CGAP_Lu24 Home sapiens cDNA clone IMAGE:3180165 similar to TR:Q13193 Q13193 CBL-B TRUNCATED FORM 2. ;, mRNA sequence.
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Pred. No. 2.4e-119;
0; Mismatches 30;
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GI:4901882
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                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL, send email to:
infoelimage.lln.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 508.
                                                                                                                                                                                                                                                                                                                                                                                                          1...52

/crganism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3180165"

/clone="Inhace:acroinoid"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NoT_CGAP_Lus was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridiatation reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fetima Bonaldo. "84 t
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Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 522)

NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Tumor Gene Index

Oppublished (1997)
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. Cons. Library Preparation: Life Technologies, Inc. Cons. Library Preparation: Life Technologies, Inc. Cons. Library Preparation: Life Technologies, Inc. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.ilnl.gov/bbrp/lmage.html
Seq primer: -400P from Gibco
High quality sequence stop: 381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 530)

NCI-CGAP. http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP. http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Onpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov.
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1022 agctgcagctctactggggccatggactccacatttgagctctgcaagatctgtgctgaga 1081
                                                                                                                                                                                                                                                                                                                         AI690580 530 bp mRNA EST 27-MAY-1999 tq02a11.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207612 similar to TR:Q13193 Q13193 CBL-B TRUNCATED FORM 2. ;, mRNA
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/db_xref="taxon:9606"
/clone="IMAGE:2207612"
/clone_lib="NCI_cGAP_U13"
/tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
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tive 0; Mismatches 2;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Onpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301, 496-1550
Email: Robert_Strausberg@nih.gov_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE198430 533 bp mENA EST 26-JUN-2000 ug78e05.yl Soares_manmary_gland_NMLMG Mus musculus cDNA clone IMAGE:1548512 5' similar to gb:X57110 PROTC-ONCOGENE C-CBL (HUMAN
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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        aggoogtgagtatotaccagttccacggtcaggotactgotgaggactcagggaacagca 1261
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Length

34; DB

68; / Score 411.4;

Query Match

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Dukaryota: Butheria; Eutheria; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 398)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Tumor Gene Index

Toll (1997)

Contact: Robert Strausberg@nih.gov

Tel: (301) 496-1550

Email: Robert Strausberg@nih.gov

Tel: (301) 496-1550

Email: Robert Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiMI at:

www-bio.llnl.gov/bbrp/image/image.html

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Seq primer: -40UP from Gibco

High quality sequence stop: 359.

Location/Qualifiers

S Location/Qualifiers
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A1368345 GI:4137990
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                       16;
ed. No. 5e-86;
Mismatches
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63108

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source

BASE COUNT ORIGIN

1192

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1312

1432

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Email: estéwatson.wustl.edu
WARWING: There is evidence that suggests that the 384-well parent
plate of this cone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible:reversed clone: similarity on wrong strand Seq primer: -4.0Ml3 fwd. from Amersham High quality sequence stop: 367.
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          Washington University School of Medicine
H444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 393.6; DB 1
95.3%; Pred. No. 7.1e-82;
Live 0; Mismatches 18
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AW463722
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1. .398
//organism="Homo sapiens"
//db_xref="taxon:9606"
/clone="InAGE:1991273"
/clone=lib="NoI_GAP_Ut3"
/clone=lib="NoI_GAP_Ut3"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab.host="DBH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
1125 c 129 g 83 t
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 462)

Hillider,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore, N., Mortis, M., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,T., Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags

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IMAGE:526956 3' similar to TR:G862411 G862411 CBL-B TRUNCATED FORM
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                                                                                                                                                                                                                                                                                                            DB 10; Length 398;
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                                                                                                                                                                                                                                                                                                          Score 396.4; DB 10;
Pred. No. 1.5e-82;
0; Mismatches 1;
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Best Local Similarity 99.7
Matches 397; Conservative
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Gaps

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ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

ACCESSION VERSION

AA113289/c LOCUS DEFINITION

38

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AA112513'
AA112513,1 GI:1665062
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KEYWORDS
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AA112513
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                                                                                                                                                                                                                                                                                   61801, USA
Tal: 217 363 5998
Fax: 217 244 5617
Email: h-lewin6uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Fescarch Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi a
cross_match from Washington University Genome Center PHRAP suite.
PCR PRimers
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                 1 (bases 1 to 440)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: placenta; Vector: p1713Pac; Site_1: BcoRI; Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                              H
BP230013B10F1 Soares normalized bovine placenta Bos taurus cDNA
clone BP230013B10F1 5', mRNA sequence.
AW463722
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Bovine ESTS

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

W. M. Keck City of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
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Pred. No. 1.5e-76;
0; Mismatches 42; Indels
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Bos taurus
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Matches 396)
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                                                                                                                                                                                AUTHORS
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 435)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Glish,W., Hawkins,M., Patrich,N., Pange,C., Rikkin,L., Mardis,E., More,M., Multman,M., Rucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., More,M., Moriberg,M., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                          AA112513 435 bp mRNA EST 23-DEC-1997 zm28c07.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:526956 5' similar to gb:x57110 PROTO-ONCOGENE C-CBL (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: estewatson wustl.edu
MARNING: There is evidence that suggests that the 384-well parent
MARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primar: -25M13 rev2 from Amersham High quality sequence stop: 336.

Location/Qualifiers
                                                                                                         ototgoagotgotgoctggotgoctggoagoactoggacagocagacotgococttctgc 1179
                              1060 ctctgcaagatctgtgctgagagcaacaaggatgtgaagattgagccgtgcgggcacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Bmail: est@watson.wustl.edu
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Best Local Similarity 89.43
Matches 362; Conservative
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B
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Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Email: smithdemail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
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H
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1 (bases 1 to 428)
Smith,T.P.L., Cassas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                       1015 gaggagcagctgcagctctactgggccatggactccacatttgagctctgcaagatctgt 1074
                                                                                                                                                                                                                                                                                                                                               61 ATCGNTATIGIGAGCICAGAIGGCAGCAICCIGCAGACCAICCCIGCCAACAAACCCIG 120
                                                                                                                                                                      775 agggacaagccaggcagttacatcttccggcccagctgtactcgcctgggggcagtgggcc 834
                                                                                                                atoggctatgtgagctdagatggcagcatcctgcagaccatccctgccaacaacccctg 894
                                Gaps
                                                                       07-JUL-2000
                                                                                                                                                                                                                                cacaacccagacctgactgagctcggccaggcagaaccccagcagcgcatccacgtgtca
                                                                                                                                                                                                                                                                                                         4
   Length 435;
                                Indels
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59653 MARC 4BOV Bos taurus cDNA 5', mRNA seguence.
AW426122
                                                                                                                                                                                                                                                                                                                                                                                                      1135 ctggctgcctggcagca----ctcggacagccagacctgcccctt 1175
                                                                                                                                                                                                                                                                                                                                                                                                                       || | CTTGGCTTGGCAGAACTTCGGACAGCCAGACCTTGCCCT 405
                              20;
   DB 1;
23.0%; Score 356.2; DB 1
94.1%; Pred. No. 3.9e-73;
ive 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_llb="marc 4Bov"
/tissue_type="pooled"
/lab_host="bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATCACCAT
BACKKARD: GTTTCCCAGTCACGACG
Plate: 27 row: I column: 8
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
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EST.
                              Conservative
               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
Query Match
Best Local Simi
Matches 381;
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AW426122
                                                                                                                835
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Tunor Gene Index
Institute, Cancer Genome Anatomy Figject (CARF),
Tunor Gene Index
Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1560
Tel: (301) 496-1560
Tel: (301) 496-1560
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Parayed by: Greg Leennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1575
Seq primer: -400P from Gibco.
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
./note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 20 and day 40 embryos." 121 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleöstomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases: 1 to 258)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                           709 gtcaaccaccnaggctacatggccttcctcacctatgatgaggtccaagagggtctgcag 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccctgtcccaggtgctcctggagggacagaaggacggttctacctctacccagatgga 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 ACTITCAGAGACAAGCCAGGCAGCTACATCITCGGGCCCAGCTGCACCTGGGGAAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 cccrcrrccagarccrcragaagacagaaggaaggcrrcraccragarggg 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 AAGAACCACAAACCGGACCIGACCGAACTCIGCCACAIGGAACGGCAIGAGCAACAACAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769 gootgoagggacaagcoaggcagttacatottooggcocagotgtactogcotggggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgggccatcggctatgtgagctcagatggcagcatcctgcagaccatccctgccaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 TGGGCCATCGGATACGTGAGCTCAGACGGCAGCATCTTGCAGACCATCCCTCTAGAAA
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0
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                                                                                                                                                                                                                                        Score 336.2; DB 2
Pred. No. 1.8e-68;
0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI758472
AI758472.1 GI:5152195
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Fri Dec

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F22931 491 bp mRNA EST 01-APR-1998 SSC17A01 Porcine small intestine cDNA library Sus scrofa cDNA clone c17a01 5', mRNA sequence.
F22931 .
F22931.1 G1:2578544
 /db_xref="taxon:9606"
/clone="IMAGE:2185170"
/clone=lib="NOI_GGAP_GBa6"
/clone_lib="NOI_GGAP_GBa6"
/lasue_type="poorly differentiated adenocarcinomia with signet ring cell features"
/lab_host="DH10B"
/clote="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Cote="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Salte_2: NotI; Cloned unidirectionally. Primer: Oligo dT: Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (Dases 1 to 491)
Wintero, A.K., Fredholm, M. and Davies, W.
Evaluation and characterization of a porcine small intestine CDNA library: analysis of 839 clones
Mamm. Genome 7 (7), 509-517 (1996)
                                                                                                                                                                                                                                                                                                  1293 gcaggtgcccctttcggctcctccattgccccacggccagatctgcccccaggaagcc 1352
                                                                                                                                                                                                                                                                                                                                                                                                                               1413 accccaggaccctgccccggcctgaaggccagggcaccagatgtgctgctcaagggagc 1472
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                                                                                                                                                                                                                                                                                                                        188 CAGAAATGCCCAGCCGAAAGTGAGACTCCTAAAGGGGAACTCCCCTCCAGCTGCGCTGGG
                                                                                                                                                                                                                                    Length 248;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                    Query Match 15.3%; Score 236; DB 13; Best Local Similarity 100.0%; Pred. No. 4.5e-45; Matches 236; Conservative 0; Mismatches 0;
                                                                                                                                                                        53 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="c17a01"
                                                                                                                                                                      87 9
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/db_xref="taxon:9606"
/clone="IMAGE:2278445"
/clone=lib="NCI_CGAP_Ut3"
/tissue_lip="poorly-differentiated endometrial
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
/note_="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541.018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1271 aaggcagggaqttggaqctggggcaggtgccctttcggctcctccattgccccacggc 1330
                                                                                                                                                                                                                                                                                                                                                                                      1331 cagatotgococccaggaagcoccagaaatgoccagocgaaagtgagactoctaaagggga 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                       actecectecagetgegetgggaececaggaecetgeeeeggeetgaaggeeagggaee 1450
                                                                                                                                                                                                                                                                                                                                                     258 AAGGCAGGGAGTTGGAGCTGGGGCAGGTGCCCTTTCGGCTCCTCCATTGCCCCCACGGC 199
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0
                                                                                                                                                                                                                                                          Length 258;
                                                                                                                                                                                                                                                                                         Indels
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Location/Qualifiers
1 248
/organism="Homo sapiens"
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AI801220
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AI801220/c
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Ä Contact: A.K. Winteroe
Department of Animal Science and Animal Health, Division of Animal
Genetics, The Royal Veterinary and Agricultural University
Bulowsvej 13, 1870 Frederiksberg C, Denmark.
Location/Qualifiers 844 gigageicagaiggeageateeigeagaceateeeigeeaacaaecaaecaggig 903 /clone_lib="Porcine small intestine cDNA library" /note="directionally cloned cDNA in XL1-blue MRF'" 142 c 145 g 79 t 9 others Query Match
Best Local Similarity 82.0%; Pred. No. 1.1e-44;
Matches 282; Conservative 0; Mismatches 60; Indels 2;

06:14:07 2000

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Fri Dec

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204;
                                                                                          Query Match
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BE283475
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutheria;
I (bases 1 to 529)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.
Goldman,G.H., Carvalho,A.F., Matsikuma,A., Baia,G.S., Simpson,D.H.,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-CT0304-120
200-012-e10&t3=2000-02-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence store: 507.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AW857217 529 bp mRNA EST 19-MAY-2000
ESC-CT03104-120200-012-e10 CT03104 Homo sapiens CDNA, mRNA sequence.
AW857217
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                       1084 aacaaggatgtgaagattgagccgtgcggcacctgctctgcag--ctgctgcctggctg 1141
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904 ctcctggagggacagaaggacgcttctacctctacccagatggaaagacccacaa
                                                                      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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ISM Muss mouse.

House mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mans musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

RS NIH-MGC hitp://www.ncbi.nlm.nih.gov/MGC/

Institutes of Health, Mammalian Gene Collection (MGC)

AL Dupublished (1999)

AL Contact: Robert Strausbergenih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Tal: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The J.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

Clone distribution: MGC clone distribution information can be http://inage.llnl.gov

Plate: LLAM8544 row: p Column: 02

High quality sequence stop: 542.

Location/Qualifiers

Location/Qualifiers

// Strain="CECKH II (feral)"
// Ab_rref="Raxon:10090"
// Clone="IMAGE:3495025"
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Length 545;

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Search completed: December 7, 2000, 12:41:38 Job time: 24581 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Searched:

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4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AB028645 Homo sapi	AF117646 Homo sapi	AF117647 Homo sapi	X57110 Human mRNA	U87925 Drosophila	AJ223175 Drosophil	U26711 Human cbl-b	U26712 Human cbl-b	U26710 Human cbl-b	X57111 Mouse mRNA	J04169 Mouse Cas N	AC073760 Mus muscu
ID	AB028645	AF117646	AF117647	HSCCBL	DMU87925	DMAJ3175	HSU26711	HSU26712	HSU26710	MMCCBL	CASNS1	AC073760
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Query Match Length DB	1575	1584	1446	3090	2661	2529	3241	3354	3982	2808	2711	237653
Query	99.5	98.3	80.1	22.0	21.3	21.2	20.3	20.9	20.9	17.5	16.9	14.3
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Rim.M. Tezuka.T. and Yamamoto.T.

Bin.M., Tezuka.T. and Yamamoto.T.

Submitted (08-JUN-1999) to the DDBJ/EMBL/GenBank databases. Tadashi
Yamamoto. Institute of Medical Science, University of Tokyo,
Department of Oncology; Shirokanedal 4-6-1, Minato-ku, Tokyo

108-8639, Japan (E-mail:tyamamotdins.u-tokyo.ac.jp,
Tel:+81-3-5449-5301, Fax:+81-3-5449-5413)
X89223 C.elegans D
ACO14994 Drosophil
ACO10033 Drosophil
ACO21988 Homo sapi
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APO01003 Homo sapi
APO01577 Homo sapi
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AL121849 Streptomy
AL122674 Streptomy
MS5285 Suid herpes
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AL360055 Streptomy
AL157400 Homo sapi
J03527 Bovine cati
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mail9413.2-3"
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/codon_start=1
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  CEDNASLII
AC014994
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Homo sapiens long CBL-3 protein (CBL-3) mRNA, alternatively spliced
isoform, complete cds.
AF117646 I GI:4959420
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I bases I to 1884)

Reane, M. M.; Ettenberg, S. A., Nau, M. M., Banerjee, P., Cuello, M., Penninger, J. and Lipkowitz, S.

Penninger, J. and Lipkowitz, S.

Occogene 18 (22), 3365-3375 (1999)

2 chases I to 1884)

Leane, M. M.; Ettenberg, S. A., Nau, M. N., Banerjee, P., Cuello, M., Penninger, J. and Lipkowitz, S.
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         810 AAGCCAGGCAGTTACATCTTCCGGCCCAGCTGTACTCGCCTGGGGCAGTGGGCCATCGGC
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                                        /organism="Homo sapiens"
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1. 1584
Direct Submission
Submitted (04-JAN-1999) Genetics Dept, Medicine F
Bethesda: Naval Hospital, Bethesda, MD 20889, USA
Location/Qualifiers
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532 C 541 t	592	<pre>Qy 601 accattgacctcacctgcagcgggcacgttccatcttcgagttcgacgtcttcaccagg 660 </pre>	<pre>Qy 661 ctctttcagccatggccaacactcctcaagaactggcagctcctggcagtcaaccaccca 720 </pre>	721 ggctacatggccttcctcacctatgatgaggtccaagagcgtctgcaggcctgcagggac 780 	781 aagccaggcagttacatcttccggcccagctgtactcgcctggggcagtgggccatcggc 840 	841 tatgtgagctcagatggcagcatcctgcagaccatccctgccaaaaaacccctgtccag 900 	901 gigotociggaggacagaaggacgoticiacototacocagaiggaaagacocacaac 960 	961 ccagacctgactgagctcggccaggcaggaccccagcagcatccacgtgtcagaggag 1020 	1021 cagctgcagctctactgggccatggactccacatttgagctctgcaagatctggctgag 1080 	1081 agcaacaagaigtgaagaitgagccgigcgggcactgcictgcagctgctgctgctgctgct 1140	1141 gcctggcagcactcggacagccagacctgcccttctgccgctgcgagatcaagggctgg 1200 	1201 gaggccgtgagtatctaccagttccacggtcaggctactgctgaggactcagggaacagc 1260 	1261 agtgaccaggaaggcagggagttggagctggggcaggtgccctttcggctcctccattg 1	1321 ccccacggccagatctgcccccaggaagcccagaaatgcccagccgaaagtgagactc 1380	1381 ctaaaggggaactcocctcoagctgggccccaggaccctgcccggcctgaagg	1441 ccagggcacccagatgtgctgctcaagggagcccaagggctggaaggggttgtgaac 15	1501	TOS COMMINMOIOCCHAOCCIAGICIAICCA
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RPDLPPRRFRNAQPRVRLLKGNSPPAALGPQDPAPA"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ii., Ettenberg,S.A., Nau,M.M., Banerjee,P., Cuello,M.,
Pr.J. and Lipkowitz,S.
a new mammalian obl family protein
e 18 (22), 3365-3375 (1999)
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d (04-JAN-1999) Genetics Dept, Medicine Branch, DCS, NCI.
Naval Hospital, Bethesda, MD 20889, USA
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1446 bp mRNA PRI 17-JUN-1999 iens short CBL-3 protein (CBL-3) mRNA, alternatively isoform, complete cds.
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protein; structurally related to the Sli-1 protein,
encoded by the cbl gene of Caenorhabditis elegans"
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tive 0; Mismatches 3; Indels 138; Gaps
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1.148aue_type="pancreatic adenocarcinoma"
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ccaaagggaactccccccaggagcccaggacccagccgaagggctgaagg 1293 ctaaaggggaactccctccagctgggacccaggaccctgcccggcctgaagg 1440 illililililililililililililililililili	HSCCEL 3090 bp mRNA for c-cbl prote-oncogene. NA 27110.1 G1:29730 S7110.1 G1:29730 S7110.1 G1:29730 S7110.1 G1:29730 S7110.1 G1:29730 S7110.1 G1:29730 S7110.2 G1:29730 S7110.3 G1:39730 S7110.3
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VKARLOKFIHKPGSYIFRLSCTRLGGWAIGYVTADGNILQTIPHNKPLFQALIDGFRE
GFYLFPDGRNQNPDLIGLCEPTPODHIKVTGEQYELYCEMGSTFQLCKICAENDKDVK
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LSSEIENLMSQGYSYQDIQXALVIAQNNIEWAKNILREFVSISSPAHVAT"

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Daga.A., Maisner.H., Banerjee,U. and Czech,M.P.
Direct Submission
Submitted (30-JAN-1997) Molecular, Cell and Developmental Biology,
University of California, Los Angeles, CA 90095, USA
Location/Qualifiers
1370 IGGCAGGAATCAGAAGGTCAGGGCTGTCCTTTCTGCCGATGTGAAATTAAAGGTACTGAA 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Droscophila melanogaster
Enkaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 2661)
Melsner, M., Daga, A. Buxton, J., Fernandez, B., Chawla, A.,
Banerjee, U. and Czech, M.P.
Interactions of Drosophila Cbl with epidermal growth factor
receptors and role of Cbl in R7 photoreceptor cell development
Mol. Cell. Biol. 17 (4), 2217-2225 (1997)
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/db_xref="G1:1842453"
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./db_xref="taxon:7227"
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/gene="D-cb1"
/codon_start=1
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Lime, G.R.

Direct Submission

Submitted (122-1997) Hime G.R., Trescowthick Research
Laboratories, Peter MacCallum Cancer Institute, Locked Bag 1, A
Beckett St., Melbourne VIC, 3000 AUSTRALIA
2 (Bases 1 to 2129)
Hime, G.R., Dhungat, M.P., Ng, A. and Bowtell, D.D.
D-Cbl, the Drosophila homologue of the c-Cbl proto-oncogene,
interacts with the Drosophila EGF receptor in vivo, despite lacking
C-terminal adaptor binding sites
0ncogene 14 (22), 2709-2719 (1997) (1402 1522 1047 1107 1164 1102 1162 1222 1282 807 867 927 987 982 cbl gene; proto-oncogene.
fruit fly.
Ellit fly.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.
(bases 1 to 2529) 627 aagaactggcagctcctggcagtcaaccaccaggctacatggccttcctcacctatgat CGCAACTGGCAGATTCTGGCCGTCACACATCCGGGCTACGTGGCGTTTCTCACATACGAC gtgtccatcttcgagttcgacgtcttcaccaggctctttcagccatggccaacactcctc 1103 GAGGIGAAGGCICGCCIACAGCGCIACAICCICAAGGCGGGCAGCIACGIITIICCGGCIC 1283 TICTACTIGIACCAGAIGGCCAAGAIGGAATCCGGATCTGTCGTCGTCGTCAAAGT 1343 CCCACAGAGGACCACATAACCGTTACCCAAGAGCAATACGAACTATACTGTGAAATGGGC tecacatttgagetetgeaagatetgtgetgagageaacaaggatgtgaagattgageeg tgcgggcacctgctctgcagctgctgctggctgcctggca---gcactcggacagccag 983 AITICCAACIICGAGGIICGAGGICIICACACGCCTCIICCAGCCTIGGGIGACACIGCIA gaggtccaagagcgtctgcaggcctgcagggacaagccaggcagttacatctccggccc agctgtactcgcctgggggcagtgggccatcggctatgtgagctcagatggcagcatcctg cagaccatccctgccaacaacccctgtcccaggtgctcctggagggacaggacggc 988 gaaccccagcagcgcatccacgtgtcagaggagcagctgcagctctactgggccatggac gaaccaggetgeacageetggeettgegeaceaccattgaeeteaeetgeagegggeac INV cbl gene. acctgoccottctgccgctgcgagatcaagggctggga 1202 1523 GGCTGCCCTTCTGTCGGGCCGAAATCAAGGGCACCGA 1560 for DMAJ3175 2529 bp mRNA Drosophila melanogaster mRNA AJ223175 AJ223175.1 GI:2739272 Location/Qualifiers 1. .2529 RESULT 6 DMAJ3175 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE FEATURES REFERENCE AUTHORS TITLE JOURNAL 1108 1043 1165 568 923 688 748 808 868 δý g QΫ́ D qq Db 쉼 qq g ΩŽ Ω δ ٠à g δ d δ g QΫ́ δ qq ö

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Pred. No. 3.9e-51;
0; Mismatches 334; Indels
                                                                                                                /protein_id="CAA11149.1"
/db_xref="G1:2739273"
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/dev_stage="embryonic"
/map="66C"
/clone="pBluescript-1255"
328. 1674
/gene="cbl"
/organism="Drosophila
/db_xref="taxon:7227"
                                                                                328. 1674
/gene="cbl"
/codon_start=1
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ilarity 61.6%;
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VNGRHSRVGSDPVLMRKHRRHDLPLEGAKVFSNGHLGSEEVDVPPRLSPPPVTTLLP
SIKCTGPLANSLSEKTRDPVEEDDDEYKIPSSHPVSLNSQPSHCHNVKPPVRSCDNGH
CMLNGTHGFSSEKKSNIPDLSIYLKGDVFDSASDPVPLPPARPPTRDNPKHGSSLNRT
PSDVDLLIPPLG"
668. 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="binds SH3 proteins; similar to c-cbl proto-oncogene
product, Swiss-Prot Accession Number P22681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MANSMNGRNPGGRGGNPRRGRILGIIDAIQDAVGPPKQAAADRR
VEKTWRLMDSKVRLQONFKLOLKNSPPYILDIIPDTYQHIRTLILSKYDDNQKLAQLS
ENBYFKIYIDSLAMKSRRAIRLFREGRERWTEDQOSDRNLFKLSLIFSHMLABIKAI
FPNGQFQGDNFRLIFKADAAEFWRKFFGDKTIVPWKVFRQCLHEVHQISSSLEAMALKA
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SYRGSVIFRLSCHRLGOWALGYYDGDNILQYIPHRKPLFQALIDGSREGFYLTPDG
RSYNDPLIGLCEPTBHHKIVTOGOYELYCEWGSTFQLCKICARNDKDVKIEPGGHLM
CTSCLTAWQESDGQGCPFCRCEIKGTEPLIYDPFDPRDEGSRCCSIIDPFGMPMLDLD
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Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete
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PRLDLIQKG1VRSPCGSPTGSPKSSPCMVRKQDRPLPAPPPLRDPPPPRPPFRPPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning and characterization of cbl-b: a SH3 binding protein with homology to the c-cbl proto-oncogene Oncogene 10 (12), 2367-2377 (1995) 95303504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3241)
Keane, M.M., Rivero-Lezcano, O.M., Mitchell, J.A., Robbins, K.C. and
Lipkowitz, S.
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5101, Bethesda Naval
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gaaccccagcagcgcatccacgtgtcagaggagcagctgcagctctactgggccatggac
                                                                         tecacatttgagetetgeaagatetgtgetgagageaacaaggatgtgaagattgageeg
                                                                                                  CCCACAGAGGACCACATAACCGTTACCCAAGAGCAATACGAACTATACTGTGAAATGGGC
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323. .2755
/note="binds SH3 proteins; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipkowitz,S., Reane,M.M. and Mitchell,J.A.
Lipkowitz,S., Reane,M.M. and Mitchell,J.A.
Direct Submission
Examitted (10-MAY-1995) Stan Lipkowitz, Navy I
Branch, National Cancer Institute, Blg 8, RM
Hospital, Bethesda, MD 20889, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xxef="taxon:9606"
/cell_line="breast cancer cell line
/map="3q"
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/product= cb1-b truncated form 1"
/protein_id="AAB09292.1"
/db_xref="GI:862409"
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1 U26711.1
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source

FEATURES

CDS

DEFINITION

HSU26711

ACCESSION VERSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE REFERENCE

TITLE JOURNAL AUTHORS

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/note="alternative splice at nucleotide 2751 truncates protein before leucine zipper" 758 c 720 g 856 t
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                                                                                                                                                                                                                                                                      DB 91; Length 3241;
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/note="encodes nuclear localization signal"
1439. .1558
/note="encodes ring finger"
2751
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Pred. No. 2e-50;
0; Mismatches 3
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ilarity 59.4%;
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Human cbl-b mRNA, complete cds:
U26710 U26710.1 GI:862406
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/note="similar to c-cbl proto-oncogene product, Swiss-Prot
Accession Number P22681"
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/protein_id="AAB09293.1"
/db_xref="G1:862411"
/translation="MANSMNGRNPGGRGGNPRKGRILGIIDAIQDAVGPPKQAAADRR
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                                                                                                                                                                                                                                                      HSU26712 3354 bp mRNA PRI 30-SEP-1996
Human cbl-b truncated form 2 lacking leucine zipper mRNA, complete
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3354)
Kasne, M., Rivero-Lezcano, O.M., Mitchell, J.A., Robbins, K.C. and
Lipkowitz, S.
Cloning and characterization of cbl-b: a SH3 binding protein with
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                                                                        1639 TGACCCCTTTGGCATGCCGATG 1660
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   859 TGAATTCTGGAGAAAGTTTTTTGGAGACAAAACTATGGAAGTATTCAGACA
                                                                                                  543 cctcctgggcacctgccaccctgtggaaccaggctgcacagccctggccttgcgcaccac
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TVBKTWKLMDKVVRLCQNFKLQLKNSPPYILDILPDTYQHLRLILSKYDDNGKLAQLS
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TUBYRKIYIDSLMKKSRRATEREKOSOORRNITKLSLLFSHMLABIRAI
FPNGOFGONFRITRADAABEWRKFPGDKTYPWKVFRQCHBVHQISSSLEAMALKS
TTOLICNDYISVFEFDIFTRLEQPMGSILRNWFLAVTHPGYMAFLYDDFVKARLQKY
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PRLDLIQKGIVRSPCGSPTGSPRSSPCMYRKQDKPLPAPPPPLADPPPPERPPPIP
PDNRLSRHIHHVESVPSRDPPMPLEAWCPRDVFGTNQLVGCRLLGEGSPKPGITASSN
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STGYGGPLABKLSEKTRDPVBEDDDEYFLDSSHPVSLANGSPGTHUNKRPVRSPVRSCDNGH
CMLNGTHGFSSEKKRN IPDLS TYLGDVFDSASDPVBLPPARPFTRDNFKHGSSLNRT
PSDYDLLIPPLGEDAFDALPPSLPPPPPARHSLIEHSKPPGSSSRPSSGQDLFLLPS
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RSYNPDLIGLCEPTPHDHIKVTGEGYELYCEMGSTFQLCKICAENDKDVKIEPCGHLM
CTSCLTAWQESDGGGCPFCRCEIKGTEPILVDPFDPRDEGSRCCSIIDPFGMPMLDLD
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PEIHHRKPHGPEAALENVDAKIAKLMGEGYAFEEVKRALEIAQNNVEVARSIIREFAF
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Lipkowitz,S., Keane,M.M. and Mitchell,J.A.
Lipkowitz,S., Keane,M.M. and Lipkowitz, May Medical Oncology
Submitted (10-MAY-1995) Stan Lipkowitz, Navy Medical Oncology
Branch, National Cancer Institute, Blg 8, Rm 5101, Bethesda Naval
Hospital, Bethesda, MD 20889, USA
Location/Qualifiers
                                                    Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Danses 1 to 3982)
Keane, M. N., Rivero-Lezcano, O.M., Mitchell, J.A., Robbins, K.C. and Lipkowitz, Cloning and characterization of cbl-b: a SH3 binding protein with Oncogene 10 (12), 2367-2377 (1995)
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prote-oncogene product, Swiss-Prot Accession Number
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/cell_line="breast cancer cell line ZR75-1"
/map="3q"
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Pred. No. 1.8e-50;
0; Mismatches 374;
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/note="encodes leucine zipper"
/877 a 1043 t
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/db_xref="GI:862407"
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Best Local Similarity 59.4%;
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Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Euthería;
Rodentia; Sciurognathí; Muridae; Murinae; Mus.
Langdon,W.Y.
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                                                                                                          cbl oncogene; nuclear protein; oncogene cellular
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KMETIGENEYFRYFMENIMKKTKQTISLFKECKERMYEENSOPRRNITKISLIFSHMI
AELKGIFPSGLFQGDTFRITKADAAEFWRKAFGEKTIVPWKSFRQALHEVHPISSGLE
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                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 2808)
Blake,T.J. and Langdon,W.Y.
A rearrangement of the c-cbl proto-oncogene in HUT78 I-lymphoma cells results in a truncated protein Cncogene 7 (4), 757-762 (1992)
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                                                                             Submitted (01-JAN-1991) Langdon W.Y., Institute of Medical u Veterinary, Sciene, IMVS, Division of Human Immunology, Box Rundel Mall Post Office, Adelaide SA 5000, Australia (bases to 2808)

Blake T.U., Shapiro, M., Morse, H.C. III. and Langdon, W.Y. The sequences of the human and mouse c-cbl proto-oncogenes v-cbl was generated by a large truncation encompassing a proline-rich domain and a leucine zipper-like motif oncogene 6 (4), 653-657 (1991)
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/protein_id="CAA40394.1"
/db_xref="GI:50315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus'
/db_xref="taxon:10090"
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1. .2808
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Langdon, W. X.
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Draft entry and computer-readable sequence for [1] kindly submitted by W.Y.Langngdon, 02-MAR-1989. Cas NS-1 is an acutely transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agaccigactgagctcggccaggcagaaccccagcagcgcatccacgtgtcagaggagca 1022
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protein (v-cbl) gene,
651 CGAATITIGGAGAAAAGCTITIGGIGAAAAGACGAIAGICCCGIGGAAGAGCITICGACA 710
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1 (Dases 1 to 2711)
1 (Dases 1 to 2711)
1 (Dases 1 to 2711)
Norse, H.O.III.
V-Ch., an oncogene from a dual-recombinant murine retrovirus induces early B-lineage lymphomas
Proc. Natl. Acad. Sci. U.S.A. 86, 1168-1172 (1989)
89145204
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                                                                                                          711 GGCCCTGCATGAAGTGCATCCCATCAGTTCTGGGCTGGAGGCCATGGCTCTGAAGTCCAC
                                                                                                                                                                                                                                                                                                       891 TTACATGGCTTTCCTGACATACGATGAAGTGAAAGCGCGCCTGCAGAAGTTCATCCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    843 tgtgagetcagatggeageatectgeagaceatecetgeeaaeaaeeeetgteeeaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gotgoagotetactgggccatggactccacatttgagctctgcaagatctgtgctgagag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200 TGATAAGGATSTGAAGATTGAGCCCTGTGGACACCTCATGTGCACATCCTGCCTCACGTC
                                                                                                                                                                cattgaceteacetgeagegggacgtgtecatettegagttegaegtetteaceagget
                                                                                                                                                                                                                                                                           663 ettteagecatggecaacaeteeteaagaaetggeageteetggeagteaaceaeceagg
                                                                                                                                                                                                                                                                                                                                                                                  723 ctacatggccttcctcacctatgatgaggtccaagagcgtctgcaggcctgcagggacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 903 gotoctggagggacagaaggacggcttctacctctacccagatggaaagacccacaaaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1143 etggeagcaeteggaeagceagaeetgeeeettetgeegetgegagateaagggetggga
                                                         543 cetectggggaacetgceaccetgtggaaceaggetgcacagcectgggcettgcgcaccac
                                                                                                                                                                                                                    771 TATTGATCTGACCTGCAATGATTATATTTCTGTCTTTGAATTTGATATTTTACACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gecaggeagttacatetteeggeeceagetgtactegeetggggeagtgggeeateggeta
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J04169.1 GI:323269
gag:onc fusion protein; viral oncogene.
GAS NS-1 retrovirus DNA, isolated from mopreviously infected with Cas-Br-M virus.
Cas NS-1 murine leukemia virus
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/ DOCUMENT OF A SA A 2885.1"

/ AD. XTEEF "GT: 323270"

/ LTAINSTALTION "LERIKEED SOUPPYDED POGGET IN VSMSFIMOS A PDIGRKLERLE
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murine retrovirus that induces pre-B and pro-B cell lymphomas. It was generated from the ecotropic Cas-Br-M virus by sequential recombinations with endogenous retroviral sequences and a cellular onocogene. The position of the oncogene junction was determined to be in the gag gene for pl0 at a position that removed the terminal 24 gag-encoded amino acids. The gag-onc duston protein appears to be responsible for fibroblast and pre-B cell transformation. The authors call this oncogene v-cbl for Casitas B-lineage lymphoma.
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                                                                                                                                                                                       Location/Qualifiers
1. .2711
/organism="Cas NS-1 murine leukemia virus"
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                                                                                                                                                                                                                                                                                                                   /note="gag-onc fusion protein"
/codon_start=2
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Consensus quality: 225699 bases at least Q40
Consensus quality: 235812 bases at least Q30
Consensus quality: 235812 bases at least Q30
Consensus quality: 235863 bases at least Q30
Consensus quality: 235863 bases at least Q30
Consensus quality: 235863 bases at least Q30
Batimated insert size: 236653; sum-of-contigs estimation
Quality coverage: 7.5 in Q20 bases; agarose-fp estimation

**NOTE: This is a 'working draft' sequence. It currently

**Consists of 16 contigs. Gaps between the contigs estimation.

**NOTE: This is a 'working draft' sequence. It currently

**Consists of 16 contigs. Gaps between the contigs estimation.

**This sequence as runs of N. The order of the pieces

** provided by the submittor.

** This sequence will be replaced

** by the filished sequence as soon as it is available and

** the accession number will be preserved.

** 1309 1409 gap of unknown length

** 1409 13300: contig of 1808 bp in length

** 41605 48203: contig of 18076 bp in length

** 41605 48203: contig of 18078 bp in length

** 41605 48203: contig of 1808 bp in length

** 41605 48203: contig of 1809 bp in length

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** 41605 48203: contig of 1809 bp in length
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DOE Joint Genome Institute.
Direct Submission
Submitted (29-UNW-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced 91:8810377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC073760. 237653 bp DNA HTG 18-JUL-2000
Mus musculus clone RP23-33H23, WORKING DRAFT SEQUENCE, 16 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
1447 IGITACIGCCGAIGGGAACATICIGCAGACAACCCCACACAATAAACCGCTCTTCCAAGC 1506
                                                                                                                                                   1507 ACTGATTGATGGCTTCAGGGAAGGCTTCTATTTGTTTCCTGATGGACGAAATCAAAATCC 1566
                                                                               gctcctggagggacagaaggacggcttctacctctacccagatggaaagacccacaaccc
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unknown length
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                                                                                                                                                                                                                                                                                                       1567 IGACCIGACAGGIITAIGIGAACCAACICCICA 1599
                                                                                                                                                                                                                               963 agacctgactgagctcggccaggcagaacccca 995
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Center Project Name: 1749735
Center clone name: RPCI-23_33H23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata,
Mammala; Eutheria; Rodentia;
1 (bases 1 to 237653)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC073760,2 GI:9256784
HTG; HTGS_PHASE2; HTGS_DRAFT.
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Unpublished
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KHHGSTIGKMERAELKATIDLSGDDFISNFEFDVFTRLFYPFKTLIKNWQTLTTAHPG
YCAFLTYDEVKRLEKLTKKEGSYIFRLSCTRFGGWAIGTVAPDGKITYGTIPQNKSLI
QADHEGGHEGGFYIFYBNGRODINLSKLKMDVPQADRVQVTSEQYSLYCEMGTTFELCKI
CDDNRSKIK REPCGHLCAKCLANWQDSDGGNTCPFCRYETKGTINKYLIDRRFFTPV
BIEKAKNVAAAEKKLISLVPDVPPRTYVSQCSQSLLHDASNSIPSVDELDLVPPPLPP
KALGTLDTLNNSQTSSSYVNIKELENVETSGEALAQVVNRQRAFSIQAPPLPPRLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MGSINTIFHRIHRFVNGTGNNARFVPSTNNSTEALTLSPRAVPS
TVSTREIPPSRSREMPGFCSEBDRRFLLARGKRANGVVRSCHSPRILLNKUPSFEILDILP
TYSTHEMLIFTGNNDILGNNDYLKIFLESMINKCRBIIKLRFTISALIYNDGSEBRRKLI
KMSLTFSHMLFEIRALFPGGIYIEDRPRMIKKRALSSFWSHHFTKKNIVPWSTFFTALE
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elegans, to the mammalian proto-oncogene c-cbl science 269 (5227), 1102-1105 (1995)
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Pasadena, CA91125, USA
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Pred. No. 1.8e-27;
O; Mismatches 396;
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/organism="Caenorhabditis elegans"
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/gene="s11-1"
/gene="s11-1"
/gene="s11-1"
/function="negative regulator
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/clone_lib="Barstead"
/map=".20 to -24.50 map units"
65..1813
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/db_xref="GI:895767"
                                                                                                                                 Yoon, C.H.
Yoon, C.H.
Direct Submission
Submitted (28-70N-1995) C.H. Yoo
TECHNOLOSY, Div. of Biology, Par
Technolosy, Div.
                                                                                                                                                                                                                                                                                                                                                /db_xref-"taxon:6239"
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Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota: Metazoa Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases 1 to 2230)
Yoon, C. H., Lee, J., Jongeward, G. D. and Sternberg, P. W.
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                            contig of 3451 bp in length; gap of unknown length; gap of unknown length; gap of unknown length; contig of 5137 bp in length; contig of 17485 bp in length; gap of unknown length; contig of 5678 bp in length; gap of unknown length; contig of 14455 bp in length; contig of 4094 bp in length; contig of 4094 bp in length; gap of unknown length; contig of 4094 bp in length; gap of unknown length; contig of 18980 bp in length; gap of unknown length; gap of unkn
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/db_xref="taxon:10090"
/clone="RP23-33H23"
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172992:
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215114:
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the submitter.
to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071 CACTACATGAAGGCCATAAAGAAGGATTTTATATTTACCCGAACGGTAGAGATCAAGATA 1130
                                                                                                                                                                                   962 cagactgactgagtcggccaggcaggaaccccagcagcgcatccacgtgtcagaggagc 1021
                                                                                                                                                                                                                                             1022 agctgcagctctactgggccatggactccacatttgagctctgcaagatctgtgctgaga 1081
                                                                                                                                                                                                                                                             1251 ACGAGAAGAACATCAAAATTGAGCCATGTGGACATTTGCTCTGCGCAAAATGTTTGGCTA 1310
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Drosophia melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 3680)

Adams,M. and Venter,J.C.
782 agccaggcagttacatcttccggcccagctgtactcgcctggggcagtgggccatcggct
                                                                              902 igotociggagggacagaaggacggottotacototacocagaiggaaagacocaaaco
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                             951 AACCIGGAAGCIACAICITCCGGITAICAIGCACACGICCIGGACAAIGGGCAAIAGGAI
                                                             atgigagotcagatggcagcatcctgcagaccatccctgccaacaacccctgtcccagg
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/db_xref="taxon:7227"
7373 c 7329 g 10616 t
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AC014994.1 GI:6436341
HTG; HTGS_PHASE2.
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ISM Drosophila melanogaster

Eukaryotd; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryotd; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygotd; Meoptera; Endopterygota; Dippera; Brachyvera;

Muscomorpha; Ephydroidea; Drosophilade; Drosophila.

25 Mazny, D.H., Adams.C., Bailey,M., Barbaria,J., Blankenburg,K.,

Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,

Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,

Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,

Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z.,

Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferragito,D.,

Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,

Glevara,M., Barris,K., Hernandez,J., Hodgson,D., Jia,Y., Jones,M.,

Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,

Lucler,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Sparke,N., Stamps,A., Sucgang,R.,

Jabor,P., Taylor,T., Wasquez,L., Vinson,R., Stamps,A., Sucgang,R.,

Horley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D.,

Watlington,S., Weinstock,G., Yu,W., Zhou,X., Nelson,D.,

Watlington,D., Weinston,D.,

Watlington,S., Weinston,D., Weinston,D., Weinston,D.,

Watlington,D., Weinston,D., Weinston,D.,

Watlington,D., Weinston,D., Weinston,D.,

Watlington,D., Weinston,D., Weinston,D.,

Watlington,D., Weinston,D., Weinston,D.,

Watlington,D., Weinston,D.,

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Upublished
(Inpublished
(Morley,K.C.
Worley,K.C.
Direct Submission
Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 20, 2000 this sequence version replaced 9::6996835
9::6996729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30328 IGGAGGCCATGGCCCTAAAGACCACTATCGATCTTACCTGCAACGACTTCATTTCCAACT 30269
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578 gcacagocotygocttgcgcaccaccattgacotcacctgcagcgggcacgtgtccatct
                                                                                                                                                                              agctcctggcagtcaaccaccaggctacatggccttcctcacctatgatgaggtccaag
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DOSOSPOLIA melanogaster clone RPC198-315,
PROSESS ***, 75 unordered pieces.
AC010033 AC023749
HTG; HTGG_PHASE1.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project Information
Center project name: DRCJ
Center Clone name: RPC198-315
Center Clone name: RPC198-315
Center Clone name: RPC198-315
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 6210% bases at least Q40
Consensus quality: 95829 bases at least Q30
Consensus quality: 95829 bases at least Q20
Estimated insert size: 100104; sum-of-contigs estimation
Quality coverage: 1.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 75 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Db 122565 CICGCCIACAGGCTACAICCICAAGGCGGGCAGCIATITICGGCTCCCCGCACG 122624
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